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(54) Title: CA125 GENE AND ITS USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

(57) Abstract: The CA125 gene has been cloned and multiple repeat sequences as well as the carboxy terminus have been identified. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. The amino acid composition of the amino terminal extension was found to be consistent with the amino acid composition of the amino terminal domain. The molecular structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. More specifically, this invention is directed to a CA125 cDNA sequence which can be introduced into animal or human cells to achieve transcription or expression of the cDNA.

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CA125 GENE AND ITS USE FOR DIAGNOSTIC AND THERAPEUTIC INTERVENTIONS

BACKGROUND OF THE INVENTION

[0001] This application is a continuation-in-part of U.S. Provisional Application Serial No. 60/284,175 filed April 17, 2001, U.S. Provisional Application Serial No. 60/299,380 filed June 19, 2001, U.S. Non-Provisional Application No. 09/965,738 filed September 27, 2001, and U.S. Provisional Application Serial No. 60/345,180. This application is a continuation-in-part of provisional application 60/427,045 (filed November 15, 2002), all of which are hereby specifically incorporated by reference. Applicants hereby specifically claims the benefit of these prior filed applications under 35 U.S.C. § 119(e), and 120.

[0002] The present invention relates generally to the cloning, identification, and expression of the CA125 gene's glycosylated amino terminal domain, the multiple repeat domain, and the carboxy terminal domain *in vitro* and, more specifically, to the use of recombinant CA125 with epitope binding sites for diagnostic and therapeutic purposes. Additionally, the genomic DNA, a molecule encoding a 5' upstream region of CA125 and a genomic DNA sequence for the amino terminal, extra cellular repeats and carboxy terminal of CA125 has been determined.

[0003] CA125 is an antigenic determinant located on the surface of ovarian carcinoma cells with essentially no expression in normal adult ovarian tissue. Elevated in the sera of patients with ovarian adenocarcinoma, CA125 has played a critical role for more than 15 years in the management of these patients relative to their response to therapy and also as an indicator of recurrent disease.

[0004] It is well established that CA125 is not uniquely expressed in ovarian carcinoma, but is also found in both normal secretory tissues and other carcinomas (i.e., pancreas, liver, colon) [Hardardottir H *et al.*, Distribution of CA125 in embryonic tissue and adult derivatives of the fetal periderm, *Am J Obstet. Gynecol.* 163;6(1):1925-1931 (1990); Zurawski VR *et al.*, Tissue distribution and characteristics of the CA125 antigen, *Cancer Rev.* 11-12:102-108 (1988); and O'Brien TJ *et al.*, CA125 antigen in human amniotic fluid and fetal membranes, *Am J Obstet Gynecol.* 155:50-55, (1986); Nap M *et al.*, Immunohistochemical characterization of 22 monoclonal antibodies against the CA125 antigen: 2nd report from the ISOBM TD-1 workshop, *Tumor Biology* 17:325-332 (1996)]. Notwithstanding, CA125 correlates directly with the disease status of affected patients (i.e., progression, regression, and no change), and has become the "gold standard" for monitoring patients with ovarian carcinoma [Bast RC *et al.*, A radioimmunoassay using a monoclonal antibody to monitor the course of epithelial ovarian cancer, *N Engl J Med.* 309:883-887 (1983); and Bon GC *et al.*, Serum tumor marker immunoassays in gynecologic oncology: Establishment of reference values, *Am J Obstet. Gynecol.* 174:107-114 (1996)]. CA125 is especially useful in post-menopausal patients where endometrial tissue has become atrophic and, as a result, is not a major source of normal circulating CA125.

[0005] During the mid 1980's, the inventor of the present invention and others developed M11, a monoclonal antibody to CA125. M11 binds to a dominant epitope on the repeat structure of the CA125 molecule [O'Brien TJ *et al.*, New monoclonal antibodies identify the glycoprotein carrying the CA125 epitope, *Am J Obstet Gynecol* 165:1857-64 (1991)]. More recently, the inventor and others developed a purification and stabilization scheme for CA125, which allows for the accumulation of highly purified high molecular weight CA125 [O'Brien TJ *et al.*, More than 15 years of CA125: What is known about the antigen, its structure and its function, *Int J Biological Markers* 13(4):188-195 (1998)].

[0006] Considerable progress has been made over the years to further characterize the CA125 molecule, its structure and its function. The CA125 molecule is a high molecular weight glycoprotein with a predominance of O-linked sugar side chains. The native molecule exists as a

very large complex (~2-5 million daltons). The complex appears to be composed of an epitope containing CA125 molecule and binding proteins which carry no CA125 epitopes. The CA125 molecule is heterogenous in both size and charge, most likely due to continuous deglycosylation of the side chains during its life-span in bodily fluids. The core CA125 subunit is in excess of 200,000 daltons, and retains the capacity to bind both OC125 and M11 class antibodies.

[0007] Despite the advances in detection and quantitation of serum tumor markers like CA125, the majority of ovarian cancer patients are still diagnosed at an advanced stage of the disease--Stage III or IV. Further, the management of patients' responses to treatment and the detection of disease recurrence remain major problems. There, thus, remains a need to significantly improve and standardize current CA125 assay systems. Further, the development of an early indicator of risk of ovarian cancer will provide a useful tool for early diagnosis and improved prognosis.

SUMMARY OF THE INVENTION

[0008] Thus, it is an object of the present invention to provide a recombinant CA125 cDNA molecule which can be introduced into animals or human cells to achieve transcription or expression of the cDNA. The utility of knowing the DNA sequence of a specific gene is that a recombinant protein can be produced which can be used as an easily renewable source of that gene or a portion of the gene. Producing and purifying recombinant protein is easier and can produce greater quantities of protein than purifying native protein from patients. The recombinant protein can then be used to produce antibodies to the gene, both polyclonal and monoclonal. The recombinant protein can also be used as a positive control in test kits and experiments.

[0009] The genomic sequence for CA125 and a 5' upstream region has been determined. A DNA sequence showing the 5' upstream region and the amino terminal portion of the CA125 molecule is set out in Table 1 and SEQ ID NO: 1. The extracellular amino terminal domain is made of exons: Exon 1 from 2205-11679; Exon 2 from 13464-13570; Exon 3 from 16177-34419; Exon 4 from 34575-38024; Exon 5 from 38689-38800; Exon 6 from 40578-45257; Exon

7 from 47360-47395; Exon 8 from 52407-52442; Exon 9 from 52686-52744 as set out in SEQ ID NO: 1. A DNA sequence showing the extracellular repeat portion of the CA125 molecule is set out in Table 2 and SEQ ID NO: 2. The genomic repeats are made of exons: Exon R1 from 1-130; Exon R2 from 442-510; Exon R3 from 5479-5652; Exon R4 from 6301-6334; Exon R5 from 6593-6657; Exon R1 from 7558-7683; Exon R2 from 8216-8284; Exon R3 from 8877-9050; Exon R4 from 9380-9413; Exon R5 from 9675-9739; Exon R1 from 10201-10291; Exon R2 from 10524-10592; Exon R3 from 11200-11373; Exon R4 from 11722-11755; Exon R5 from 12016-12036; Exon R1 from 12169-12295; Exon R2 from 12532-12600; Exon R3 from 13219-13392; Exon R4 from 13723-13756; Exon R5 from 14016-14077; Exon R1 from 15001-15126; Exon R2 from 15367-15435; Exon R1 from 15648-15773; Exon R2 from 16002-16070; Exon R3 from 16653-16826; Exon R4 from 17158-17191; Exon R5 from 17453-17517; Exon R1 from 18532-18657; Exon R2 from 18888-18956; Exon R3 from 19633-19806; Exon R4 from 20141-20176; Exon R5 from 20387-20449; Exon R1 from 21609-21731; Exon R2 from 21940-22008; Exon R3 from 22605-22778; Exon R4 from 23109-23142; Exon R1 from 29046-29168; Exon R2 from 29266-29334; Exon R3 from 33917-34090; Exon R4 from 36702-36734; Exon R5 from 38270-38320; Exon R1 from 39104-39224; Exon R2 from 39315-39383; Exon R3 from 39532-39705; Exon R4 from 41862-41992. A DNA sequence showing the carboxy terminal domain of the CA125 molecule is set out in Table 3 and SEQ ID NO: 3. The carboxy terminal portion is made of exons: Exon C1 from 1-66; Exon C2 from 1802-1947; Exon C3 from 4198-4350; Exon C4 from 4679-4747; Exon C5 from 6811-6978; Exon C6 from 11232-11270; Exon C7 from 11594-11677; Exon C8 from 14095-14187 as set out in SEQ ID NO: 3. A full length cDNA molecule for CA125 is set out in Table 4 and SEQ ID NO: 4. A CA125 protein is set out in Table 5 and SEQ ID NO: 5.

[0010] Now that the DNA sequence which encodes CA125 has been discovered known synthetic methods can be employed to prepare DNA molecules containing portions of the sequence. Conventional cloning vehicles, such as plasmids, viruses, or bacteria phages can be modified using known methods so as to produce novel cloning vehicles which contain cDNA encoding, CA125, analogs or mutants thereof. Similarly, such cloning vehicles can be modified or engineered so that they contain DNA molecules from Table 4 and SEQ ID NO: 4 or segments

substantially similar thereto. The DNA molecule inserted may be made by various methods including enzymatic or chemical synthesis.

[0011] The CA125 gene has been cloned and multiple repeat sequences as well as the glycosylated amino terminal and the carboxy terminus have been identified. CA125 requires a transcript of more than 35,000 bases and occupies approximately 150,000 bp on chromosome 19p 13.2. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. Analysis of the amino terminal extension revealed that its amino acid composition is consistent with the amino acid composition of the amino terminal domain.

[0012] Perhaps even more significantly, the multiple repeat domains of CA125 or other domains could also be used for the development of a potential vaccine for patients with ovarian cancer. In order to induce cellular and humoral immunity in humans to CA125, murine antibodies specific for CA125 were utilized in anticipation of patient production of anti-ideotypic antibodies, thus indirectly allowing the induction of an immune response to the CA125 molecule. With the availability of recombinant CA125, especially domains which encompass epitope binding sites for known murine antibodies, it will be feasible to more directly stimulate patients' immune systems to CA125 and, as a result, extend the life of ovarian carcinoma patients.

[0013] The recombinant CA125 of the present invention may also be used to develop therapeutic targets. Molecules like CA125, which are expressed on the surface of tumor cells, provide potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. Humanized or human antibodies to CA125 epitopes could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. Natural ligands having a natural

binding affinity for domains on the CA125 molecule could also be utilized to deliver therapeutic agents to tumor cells.

[0014] CA125 expression may further provide a survival or metastatic advantage to ovarian tumor cells. Antisense oligonucleotides derived from the CA125 repeat sequences could be used to down-regulate the expression of CA125. Further, antisense therapy could be used in association with a tumor cell delivery system of the type described above.

[0015] Recombinant domains of the CA125 molecule also have the potential to identify small molecules, which bind to individual domains of the CA125 molecule. These small molecules could also be used as delivery agents or as biological modifiers.

[0016] In another aspect of the present invention, an isolated nucleic acid of the CA125 gene is disclosed, which comprises a nucleotide sequence selected from the group consisting of: (a) the nucleotide sequences set forth in SEQ ID NOS: 1, 2, 3 and 4; (b) a nucleotide sequence having at least 70% sequence identity to any one of the sequences in (a); (c) a degenerate variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

[0017] In another aspect of the present invention, an isolated nucleic acid of the CA125 gene, comprising a sequence that encodes a polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequences set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to any one of the sequences in (a); (c) a conservative variant of any one of (a) to (b); and (d) a fragment of any one of (a) to (c).

[0018] The vector may be a cloning vector, a shuttle vector, or an expression vector. A cultured cell comprising the vector is also contemplated.

[0019] More specifically, this invention relates to a purified antibody that selectively binds to an epitope in the CA125 protein of SEQ ID NO: 5. Similarly, the purified antibody selectively binds to an amino acid sequence having at least 50% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence having at least 60% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence

having at least 70% sequence identity to said sequence; the purified antibody selectively binds to an amino acid sequence having at least 80% sequence identity to said sequence; and the purified antibody selectively binds to an amino acid sequence having at least 90% sequence identity to said sequence. Additionally, purified antibody can be a conservative variant of the amino acid sequence set forth in SEQ ID NO: 5 or a fragment thereof.

DETAILED DESCRIPTION OF THE INVENTION

[0020] In accordance with the present invention, conventional molecular biology, microbiology, and recombinant DNA techniques may be used that will be apparent to those skilled in the relevant art. Such techniques are explained fully in the literature (see, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D. N. Glover ed. 1985); "Oligonucleotide Synthesis" (M. J. Gait ed. 1984); "Nucleic Acid Hybridization" (B. D. Hames & S. J. Higgins eds. (1985)); "Transcription and Translation" (B. D. Hames & S. J. Higgins eds. (1984)); "Animal Cell Culture" (R. I. Freshney, ed. (1986)); "Immobilized Cells And Enzymes" (IRL Press, (1986)); and B. Perbal, "A Practical Guide To Molecular Cloning" (1984)).

[0021] Therefore, if appearing herein, the following terms shall have the definitions set out below.

[0022] A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

[0023] A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, inter alia, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes.

[0024] As used herein, the term "gene" shall mean a region of DNA encoding a polypeptide chain.

[0025] "Messenger RNA" or "mRNA" shall mean an RNA molecule that encodes for one or more polypeptides.

[0026] "DNA polymerase" shall mean an enzyme which catalyzes the polymerization of deoxyribonucleotide triphosphates to make DNA chains using a DNA template.

[0027] "Reverse transcriptase" shall mean an enzyme which catalyzes the polymerization of deoxy- or ribonucleotide triphosphates to make DNA or RNA chains using an RNA or DNA template.

[0028] "Complementary DNA" or "cDNA" shall mean the DNA molecule synthesized by polymerization of deoxyribonucleotides by an enzyme with reverse transcriptase activity.

[0029] An "isolated nucleic acid" is a nucleic acid the structure of which is not identical to that of any naturally occurring nucleic acid or to that of any fragment of a naturally occurring genomic nucleic acid spanning more than three separate genes. The term therefore covers, for example, (a) a DNA which has the sequence of part of a naturally occurring genomic DNA molecule but is not flanked by both of the coding sequences that flank that part of the molecule in the genome of the organism in which it naturally occurs; (b) a nucleic acid incorporated into a vector or into the genomic DNA of a prokaryote or eukaryote in a manner such that the resulting molecule is not identical to any naturally occurring vector or genomic DNA; (c) a separate molecule such as a cDNA, a genomic fragment, a fragment produced by polymerase chain reaction (PCR), or a restriction fragment; and (d) a recombinant nucleotide sequence that is part of a hybrid gene, i.e., a gene encoding a fusion protein.

[0030] "Oligonucleotide", as used herein in referring to the probes or primers of the present invention, is defined as a molecule comprised of two or more deoxy- or ribonucleotides, preferably more than ten. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

[0031] "DNA fragment" includes polynucleotides and/or oligonucleotides and refers to a plurality of joined nucleotide units formed from naturally-occurring bases and cyclofuranosyl groups joined by native phosphodiester bonds. This term effectively refers to naturally-occurring species or synthetic species formed from naturally-occurring subunits. "DNA fragment" also refers to purine and pyrimidine groups and moieties which function similarly but which have non naturally-occurring portions. Thus, DNA fragments may have altered sugar moieties or inter-sugar linkages. Exemplary among these are the phosphorothioate and other

sulfur containing species. They may also contain altered base units or other modifications, provided that biological activity is retained. DNA fragments may also include species which include at least some modified base forms. Thus, purines and pyrimidines other than those normally found in nature may be so employed. Similarly, modifications on the cyclofuranose portions of the nucleotide subunits may also occur as long as biological function is not eliminated by such modifications.

[0032] "Primer" shall refer to an oligonucleotide, whether occurring naturally or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, the source of primer and the method used. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 10-25 or more nucleotides, although it may contain fewer nucleotides.

[0033] The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence or hybridize therewith and thereby form the template for the synthesis of the extension product.

[0034] As used herein, the term "hybridization" refers generally to a technique wherein denatured RNA or DNA is combined with complementary nucleic acid sequence which is either

free in solution or bound to a solid phase. As recognized by one skilled in the art, complete complementarity between the two nucleic acid sequences is not a pre-requisite for hybridization to occur. The technique is ubiquitous in molecular genetics and its use centers around the identification of particular DNA or RNA sequences within complex mixtures of nucleic acids.

[0035] As used herein, "restriction endonucleases" and "restriction enzymes" shall refer to bacterial enzymes which cut double-stranded DNA at or near a specific nucleotide sequence.

[0036] "Purified polypeptide" refers to any peptide generated from CA125 either by proteolytic cleavage or chemical cleavage.

[0037] "Degenerate variant" refers to any amino acid variation in the repeat sequence, which fulfills the homology exon structure and conserved sequences and is recognized by the M11, OC125 and ISOBM series of antibodies.

[0038] "Fragment" refers to any part of the CA125 molecule identified in a purification scheme.

[0039] "Conservative variant antibody" shall mean any antibody that fulfills the criteria of M11, OC125 or any of the ISOBM antibody series.

[0040] "Homology" refers to similarity based on identical base matches in alignment. When two sequences are identical there is a 100% homology, as base matches differ in alignment the homology between two sequences is reduced.

[0041] The CA125 gene has been cloned and multiple repeat sequences as well as the carboxy terminus have been identified. The genomic DNA for the CA125 gene is set out in SEQ ID NO: 4. The CA125 molecule comprises three major domains: an extracellular amino terminal domain (Domain 1); a large multiple repeat domain (Domain 2); and a carboxy terminal domain (Domain 3) which includes a transmembrane anchor with a short cytoplasmic domain. The amino terminal domain is assembled by combining five genomic exons, four very short amino terminal sequences and one extraordinarily large exon. This domain is dominated by its capacity

for O-glycosylation and its resultant richness in serine and threonine residues. Additionally, an amino terminal extension is present, which comprises four genomic exons. The amino acid composition of the amino terminal extension was found to be consistent with the amino acid composition of the amino terminal domain. The molecular structure is dominated by a repeat domain comprising 156 amino acid repeat units, which encompass the epitope binding sites. More than 60 repeat units have been identified, sequenced, and contiguously placed in the CA125 domain structure. The repeat units encompass an interactive disulfide bridged C-enclosure and the site of OC125 and M11 binding. The repeat sequences demonstrated 70-85% homology to each other. Expression of the repeats was demonstrated in *E. coli*. The CA125 molecule is anchored at its carboxy terminal through a transmembrane domain and a short cytoplasmic tail. The carboxy terminal also contains a proteolytic cleavage site approximately 50 amino acids upstream from the transmembrane domain, which allows for proteolytic cleavage and release of the CA125 molecule. Any one of the repeat domains has the potential for use as a new gold standard for detecting and monitoring the presence of the CA125 antigen. Further, the repeat domains or other domains, especially the c-terminal to the repeat domain also provide a basis for the development of a vaccine, which would be useful for the treatment of ovarian cancer and other carcinomas where CA125 is elevated.

[0042] The DNA sequences of the present invention can also be characterized as encoding the amino acid sequence equivalents of the amino acid sequence, equivalents, as used in this context, include peptides of substantially similar length and amino acid identity to those disclosed, but having conservative amino acid substitution at a non-critical residue position. A conservative amino acid substitution is a substitution in which an amino acid residue is replaced with an amino acid residue of differing identity, but whose R group can be characterized by chemically similar. Four common categories include: polar but uncharged R groups; positively charged R groups; negatively charged R groups; and, hydrophobic R groups. A preferred conservative substitution involves the substitution of a second hydrophobic residue for a first hydrophobic residue, the first and second hydrophobic residues differing primarily in the size of the R group. The hydrophobic residue would be predicted to be located internally in the folded peptide structure and the mild perturbation caused only by a change in the size of an R group at

an internally located which would not alter the antigenicity of R protein. More specifically, two nucleic acid molecules are substantially equivalent if they have at least about 70% homology.

[0043] The isolated cDNA sequences (Table 4 and SEQ ID NO: 4) of the present invention can be inserted into an expression vector. Such vectors contain all necessary regulatory signals to promote the expression of a DNA sequence of interest. Expression vectors are typically either prokaryote or eukaryote specific. Expression vectors can be introduced into either prokaryote or eukaryote cells to produce CA125 proteins or portions thereof. The isolated cDNA sequence as shown in Table 4 was expressed to provide the CA125 molecule set out in Table 5 and SEQ ID NO: 5. The expressed CA125 is a polypeptide with the amino acid sequence set forth in SEQ ID NO: 5; an amino acid sequence having at least 50% sequence identity to the sequence, a conservative for variant or a fragment of any of the above. Two polypeptide sequences are substantially equivalent if there is at least 50% sequence homology and substantial similar physical characteristics. However, in practice, a portion of an isolated nucleic acid molecule set out in SEQ ID NO: 4 is expressed to obtain a fragment of the CA125 molecule. This fragment is then purified to obtain an isolated CA125 fragment.

[0044] In certain embodiments, "purified" refers to a polypeptide composition which has been subjected to fractionation to remove various nonprotein components such as other cellular components. Various techniques suitable for use in protein purification are known to those skilled in the relevant art. These techniques include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combination of such techniques. Similarly, a "purification scheme" is a technique or system to remove various nonprotein components such as other cellular components from the expressed protein. Various techniques suitable for use in protein purification are known to those skilled in the relevant art. These techniques include, for example, precipitation with ammonium sulphate, PEG, antibodies and the like or by heat denaturation, followed by centrifugation; chromatography steps such as

ion exchange, gel filtration, reverse phase, hydroxylapatite and affinity chromatography; isoelectric focusing; gel electrophoresis; and combination of such techniques.

[0045] The genomic DNA and a full-length cDNA sequence of human CA125 has been determined. Additionally, a nucleic acid molecule encoding a 5' upstream region of the CA125 gene has been determined. cDNA is expressed with the use of an expression vector. An expression vector is a carrying vector that has an inducer for expression built into the vector. Different vectors use different inducers. The cDNA is ligased into the expression vector using restriction digest sites designed in the vector. The cDNA must be ligased in the sense direction and in the correct reading frame for expression to occur. Once the cDNA is ligased into the expression vector, the construct is transformed into a cell. In the preferred embodiment, we use E-Coli bacteria, but the transformation can be done with yeast, mammalian cells, plants cells, etc. The transformed cells are then grown in culture and protein production is induced with the an inducing agent for the expression vector. In the preferred embodiment, we use the pQE-30 expression vector and induce with IPTG. Once induction has occurred, the cells are harvested and the protein is purified. It should be noted that some expression vectors add tags to the recombinant protein to aid in purification. For example, pQE-30 adds a His-Tag which binds to nickel to aid in purification. Once cells have been successfully transformed, a small aliquot can be frozen and stored for future use.

[0046] With a cDNA sequence, one skilled in the art has an easily renewable source of purified CA125. Portions of this cDNA sequence can be expressed to make CA125 polypeptides and these polypeptides can be used to make monoclonal antibodies. These monoclonal antibodies can be made by one skilled in the art to portions of the protein which heretofore do not have any monoclonal antibodies, such as the amino terminal sequence.

[0047] More specifically, the purified antibodies are made by the following process: the recombinant protein is injected into an animal (usually a mouse, but other animals can be used). The animal's B-lymphocytes produce antibodies to the protein. Each activated B lymphocyte forms a clone of cells in spleen or lymph nodes, with each cell of the clone producing identical antibody. These spleen cells are then harvested and fused with myeloma cells to produce

hybridomas. These hybridomas are immortal and produce only one type of antibody. The hybridomas are selected from cells that did not fuse by selective media. The hybridomas can then be grown in large quantities to produce large quantities of monoclonal antibodies.

[0048] **Therapeutic Targets:** Molecules, which are expressed on the surface of tumor cells as CA125 is, offer potential targets for immune stimulation, drug delivery, biological modifier delivery or any agent which can be specifically delivered to ultimately kill the tumor cells. CA125 offers such potential as a target: 1) Antibodies to CA125 epitopes or newly described potential epitopes: Most especially humanized or human antibodies to CA125 which could directly activate the patients' immune system to attack and kill tumor cells. Antibodies could be used to deliver all drug or toxic agents including radioactive agents to mediate direct killing of tumor cells. 2) Natural ligands: Under normal circumstances, molecules are bound to the CA125 molecule e.g. a 50 k dalton protein which does not contain CA125 epitopes co-purifies with CA125. Such a molecule, which might have a natural binding affinity for domains on the CA125 molecule, could also be utilized to deliver therapeutic agents to tumor cells.

[0049] **Anti-sense therapy:** CA125 expression may provide a survival or metastatic advantage to ovarian tumor cells as such antisense oligonucleotide derived from the CA125 sequence could be used to down-regulate the expression of CA125. Antisense therapy could be used in association with a tumor cell delivery system such as described above.

[0050] **Small Molecules:** Recombinant domains of CA125 also offer the potential to identify small molecules which bind to individual domains of the molecule. Small molecules either from combinatorial chemical libraries or small peptides can also be used as delivery agents or as biological modifiers.

[0051] **Transgenic Animals/Transformed:** CA125 and genomic DNA can be used to develop transgenic animal models and can be used under low stringency conditions, to clone CA125 cDNAs and genomic DNAs of other animal species. The CA125 cDNA can be used to prepare stable transformants. The bacterial cells could be transformed with CA125 cDNA to include these genes.

Example 1

[0052] Expression of 6xHis-tagged CA125 repeat in *E. coli*: The open reading frame of the CA125 repeat was amplified by PCR with the 5' sense primer 1 (5'-ACCGGATCCATGGGCCACACAGAGCCTGGCCC-3') (SEQ ID NO: 6) and the 3' antisense primer 2 (5'-TGTAAGCTTAGGCAGGGAGGATGGAGTCC-3') (SEQ ID NO: 7). The open reading frame of the CA125 repeat constitutes a portion of the isolated nucleic acid molecule set out in SEQ ID NO: 4. PCR was performed in a reaction mixture consisting of ovarian tumor cDNA derived from 50 ng of mRNA, 5 pmol each of sense and antisense primers for the CA125 repeat, 0.2 mmol of dNTPs, and 0.625 U of Taq polymerase in 1x buffer in a final volume of 25 μ l. This mixture was subjected to 1 minute of denaturation at 95°C followed by 30 cycles of PCR consisting of the following: denaturation for 30 seconds at 95°C, 30 seconds of annealing at 62°C, and 1 minute of extension at 72°C with an additional 7 minutes of extension on the last cycle. The product was electrophoresed through a 2% agarose gel for separation, the PCR product was purified and digested with the restriction enzymes BamHI and HindIII. This digested PCR product was ligated into the expression vector pQE-30, which had also been digested with BamHI and HindIII. The ligation reaction consisted of 1 μ l of 10x ligation buffer, 1 μ l of 10x bovine serum albumin (BSA), 1 μ l of T4 ligase enzyme, and 7 μ l of digested PCR product. The reaction went overnight at 15° C. This clone would allow for expression of recombinant amino-terminal 6xHis-tagged CA125 repeat. The construct was then transformed into JM109 *E. coli* cells. The transformation reaction consisted of 5 μ l of ligation reaction and 50 μ l of cells. The reaction was mixed gently and then incubated on ice for 30 minutes. The reaction was then heat shocked at 42° C for 45 seconds in a water bath before being returned to ice for 2 minutes. 500 μ l of LB broth media were added and the mixture was incubated at 37° C for 1 hour. At the end of 1 hour the cells were spun down in a microfuge at 4,000 x g for 5 minutes and approximately 450 μ l of media was removed. The cells were resuspended in the remaining 100 μ l of media, transferred to a LAIX plate, and incubated overnight at 37° C. White colonies were picked from the plate and cultured in 5ml LB broth media to determine if the transformation was successful. Transformed *E. coli* were grown in 1L cultures to an OD₆₀₀ of 1.5-2.0 at 37°C and were induced with IPTG (0.1 mM) for 4-6 hours at 25°C to produce

recombinant protein. Whole E.coli lysate was electrophoresed through a denaturing 12% polyacrylamide gel and Coomassie stained to detect highly expressed proteins. His-tagged proteins were purified under denaturing conditions using Ni-NTA agarose metal chelating affinity chromatography available from Qiagen according to the manufacturer's instructions. Cells are spun down to remove liquid LB broth media. The cells are then resuspended in 40ml of 8M Urea lysis buffer (pH 8.0) and incubated with agitation overnight at room temperature. The mixture is then spun down and the lysate is removed. The lysate is then incubated with Ni-NTA agarose beads with agitation overnight at room temperature. The beads are pelleted and the supernatant is removed. The beads are then washed twice in lysis buffer pH 8.0 plus Triton X, three times with lysis buffer pH 6.3 plus Triton X, and four times with lysis buffer pH 6.3 without Triton X. The protein is then eluted from the beads with lysis buffer pH4.2 plus 25mM EDTA incubated overnight with agitation at room temperature. The beads are pelleted and the supernatant containing the recombinant protein is removed. The supernatant is then dialyzed twice in .2x PBS to remove the urea and freeze dried for storage. 1L of culture produced 2.4mg of recombinant protein.

[0053] It should be understood that various changes and modifications to the presently preferred embodiments described herein will be apparent to those skilled in the art. Such changes and modifications can be made without departing from the spirit and scope of the present invention and without diminishing its attendant advantages.

Table 1

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

1 GGTGCGCACC ACTATGTCTG GCTAATTTTT GTATTTTTTT GTAGAGACAT
51 GGTTCACCA TGTTGGCCAG GCTGGTCTCG AATTCCTGAC TTCAAGTAAT
101 CCACCCACCT CAGCCTCCCA AAGTGCTGGG ATTACAAGCA TGAGCCACCA
151 TGCATGGCCT AAAGCTTCTT TTAAAGCCAC CAAGTCCCTT CCCATGTTAG
201 CCCACTAATC CATGGGTTAG TCATGAATGG ATTAATCTAT TCATACGGAC
251 AGAGCCCTCA TCACCCAATC ACCTCTTAAA GGCCCCACCT CTCAATACTG
301 CCACACTGGG GATTAAGTTT CAACAGAGTT TTGGAGGGGA CATTCAAATC
351 ATAGTAATGC CCAAAGTGAA AAATCTTCCC TGCACTTTTT CCTCAACAAA
401 AACAGCCAGA GATAGTGAGC TGCCAGGAAA TTCTTTTTTT TTTCCTCTTC
451 TGTCTAAAT CAGCATCGCT AGACCTTTAC ATGATTCAAC CTCATCTTCT
501 TCACCCTCTG GGTCTGTAAG TTTTATTTAT TTATTTATTA TTTTCTGGG
551 ACAGACTCTG GCTCTGTCGC CCAGGCTGAA GTGCAGTGGT GTGATCTTGG
601 CTCCTGCAA CCTCCGCCTC CCGGGTTCAA GCGATTCTCC TGCCTCAGCC
651 TCCTGAGTAG CTGGGATTAC AGGTGGGCGC CACCACACCC AGCTAATTTT
701 TTGTATTTTT AGTAGAGATG GGGTTTCACC ATATTAGCCA GGATGGTCTC
751 CATCTCTTGA CCTCGTGATC TGCCCACCTC AGCCTCCCAA AATGCTGGGA
801 TTACAGGCAT GAGACACCAC GCCCAGCAGG CCAGGGTCAT GAGATTTTAA
851 TCAAGAGCAA CTTCCACTGA TTCCTGAGAG TGCATCTGTG GGCCCTGCT
901 CTGATCTGAA CAGAAGTGCC GTGTCTTCTC TGACCTCCAC TTCTCAATTC
951 AAGAGCCTTA GTATCTGCCA GTATCACACA CTGAGCATTG GCTCCATCTC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)				
1001	ATGGGGGTGT	AGGTAGGGGC	TCTATCTGCA	TCTTTCTTTC
	TTTTTTTCTT			
1051	TCTTTCCCTT	CCTCCCTTCC	TCCTCCCTC	GGTCCTCTCT
	TTCTTTCCCT			
1101	TTCTTTCTTC	CTTCCTCCCT	TCCTCCCTCC	CTCCCTCTCT
	CTTTCTCTCT			
1151	TTCTTTCTTT	CCTTCTTTCT	TTCTTTCTCT	CTTCCTTCCC
	TCCCTCCCTC			
1201	CTTCCTTCCT	TTCTCTTTCT	TTCTCTTTCT	TTCTTTTTTT
	CCTTCCTTCC			
1251	TTCTTTCTTT	CTCTTTCTCT	CCCTCCCTTC	CTTCCTTCCT
	TCCTTCCTTC			
1301	CTTCCTTTCT	TTCTTTCTTT	CTTTCTTTCT	TTCTTTCTTT
	CTTTCTTTCT			
1351	TTCTTTCTTC	CTTCCTTCCT	TCCTTCCTTC	CTTCCTTCCT
	TCCTTCCTTT			
1401	CTTTTCTTTC	TTTCTCTTTC	TTTTTGAGAC	AGAGCTCTTA
	TTACCCATGC			
1451	TGGAGTGCAG	TGGTGTGACC	TTGGCTTACT	GCAACATCTG
	CCTCCTAGGG			
1501	TCAAGTGATT	CTCCTGCCTC	AGCCTCCTAA	GTAGCTGGGA
	TTACAGACAC			
1551	ATGCCACCAC	ACCCAATATT	TATTTTTATT	AAAATTTTTT
	TTAAAATTAT			
1601	TTTTAAAAAA	TTAAAAATAA	TTTTGTATTT	TTAGTAGAGA
	CGGGGTTTCT			
1651	CCATGTTGGT	CAGGCTGATC	TCAAACCTCC	AACCTCAGGT
	GATCCTCCCA			
1701	CCTCACCTCC	CAAAGTGCTG	GGATTACAGG	CATGAGCCAC
	CGTGCCCAGC			
1751	CTGGTTCCTG	GTTTCTAAGA	CATCACACAC	ACACACACAC
	ACACACACAC			
1801	ACACTCACAC	ACTCAGAGAG	AGAGAGAGAG	AGAGGATCAT
	TAAGACATGA			
1851	TACACTAAGA	AATTCTATTG	TGCAGACACT	GAGAATCCGT
	TAAAAAGTTT			
1901	GAAGGGAAGA	ATTGAGATCA	TCAGGTGTTT	ATTTGAGGAA
	ATTGTCTGTG			
1951	GTTGAACTAT	CCTTTCCTTT	CTCTCCCTGA	GATTTGGTCT
	TCTCAATTAG			

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

2001 AAGCGTTGCA CAATTCCTCCC AACCTCCATA CATACGGCAG CTCTTCTAGA
 2051 CACAGGTTTT CCCAGGTCAA ATGCGGGGAC CCCAGCCATA TCTCCCACCC
 2101 TGAGAAATTT TGGAGTTTCA GGGAGCTCAG AAGCTCTGCA GAGGCCACCC
 2151 TCTCTGAGGG GATTCTTCTT AGACCTCCAT CCAGAGGCAA ATGTTGACCT

Exon1

2201 GTCCATGCTG AAACCCTCAG GCCTTCCTGG GTCATCTTCT CCCACCCGCT
 2251 CCTTGATGAC AGGGAGCAGG AGCACTAAAG CCACACCAGA AATGGATTCA
 2301 GGACTGACAG GAGCCACCTT GTCACCTAAG ACATCTACAG GTGCAATCGT
 2351 GGTGACAGAA CATACTCTGC CCTTTACTTC CCCAGATAAG ACCTTGGCCA
 2401 GTCCTACATC TTCGGTTGTG GGAAGAACCA CCCAGTCTTT GGGGGTGATG
 2451 TCCTCTGCTC TCCCTGAGTC AACCTCTAGA GGAATGACAC ACTCCGAGCA
 2501 AAGAACCAGC CCATCGCTGA GTCCCAGGT CAATGGTACT CCCTCTAGGA
 2551 ACTACCCTGC TACAAGCATG GTTTCAGGAT TGAGTTCCCC AAGGACCAGG
 2601 ACCAGTTCCA CAGAAGGAAA TTTTACCAA GAAGCATCTA CATAACACT
 2651 CACTGTAGAG ACCACAAGTG GCCCAGTCAC TGAGAAGTAC ACAGTCCCCA
 2701 CTGAGACCTC AACAACTGAA GGTGACAGCA CAGAGACCCC CTGGGACACA
 2751 AGATATATTC CTGTAAAAAT CACATCTCCA ATGAAAACAT TTGCAGATTC
 2801 AACTGCATCC AAGGAAAATG CCCCAGTGTC TATGACTCCA GCTGAGACCA
 2851 CAGTTACTGA CTCACATACT CCAGGAAGGA CAAACCCATC ATTTGGGACA
 2901 CTTTATTCTT CCTTCCTTGA CCTATCACCT AAAGGGACCC CAAATTCAG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

2951 AGGTGAAACA AGCCTGGAAC TGATTCTATC AACCACTGGA TATCCCTTCT
3001 CCTCTCCTGA ACCTGGCTCT GCAGGACACA GCAGAATAAG TACCAGTGCG
3051 CCTTTGTCAT CATCTGCTTC AGTTCCTGAT AATAAAATAT CAGAGACCAG
3101 CATATTCTCA GGCCAGAGTC TCACCTCCCC TCTGTCTCCT GGGGTGCCCC
3151 AGGCCAGAGC CAGCACAATG CCCAACTCAG CTATCCCTTT TTCCATGACA
3201 CTAAGCAATG CAGAAACAAG TGCCGAAAGG GTCAGAAGCA CAATTTCCTC
3251 TCTGGGGACT CCATCAATAT CCACAAAGCA GACAGCAGAG ACTATCCTTA
3301 CCTTCCATGC CTTCGCTGAG ACCATGGATA TACCCAGCAC CCACATAGCC
3351 AAGACTTTGG CTTCAGAATG GTTGGGAAGT CCAGGTACCC TTGGTGGCAC
3401 CAGCACTTCA GCGCTGACAA CCACATCTCC ATCTACCACT TTAGTCTCAG
3451 AGGAGACCAA CACCCATCAC TCCACGAGTG GAAAGGAAAC AGAAGGAACT
3501 TTGAATACAT CTATGACTCC ACTTGAGACC TCTGCTCCTG GAGAAGAGTC
3551 CGAAATGACT GCCACCTTGG TCCCCACTCT AGGTTTTACA ACTCTTGACA
3601 GCAAGATCAG AAGTCCATCT CAGGTCTCTT CATCCCACCC AACAGAGAG
3651 CTCAGAACCA CAGGCAGCAC CTCTGGGAGG CAGAGTTCCA GCACAGCTGC
3701 CCACGGGAGC TCTGACATCC TGAGGGCAAC CACTTCCAGC ACCTCAAAAG
3751 CATCATCATG GACCAGTGAA AGCACAGCTC AGCAATTTAG TGAACCCAG
3801 CACACACAGT GGGTGGAGAC AAGTCCTAGC ATGAAAACAG AGAGACCCCC
3851 AGCATCAACC AGTGTGGCAG CCCCTATCAC CACTTCTGTT CCCTCAGTGG
3901 TCTCTGGCTT CACCACCCTG AAGACCAGCT CCACAAAAGG GATTGGCTT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

3951 GAAGAAACAT CTGCAGACAC ACTCATCGGA GAATCCACAG CTGGCCCAAC
4001 CACCCATCAG TTTGCTGTTC CCACTGGGAT TTCAATGACA GGAGGCAGCA
4051 GCACCAGGGG AAGCCAGGGC ACAACCCACC TACTCACCAG AGCCACAGCA
4101 TCATCTGAGA CATCCGAGA TTTGACTCTG GCCACGAACG GTGTCCCAGT
4151 CTCCGTGTCT CCAGCAGTGA GCAAGACGGC TGCTGGCTCA AGTCCTCCAG
4201 GAGGGACAAA GCCATCATAT ACAATGGTTT CTTCTGTCAT CCCTGAGACA
4251 TCATCTCTAC AGTCCTCAGC TTTCAGGGAA GGAACCAGCC TGGGACTGAC
4301 TCCATTAAAC ACTAGACATC CCTTCTCTTC CCCTGAACCA GACTCTGCAG
4351 GACACACCAA GATAAGCACC AGCATTCCTC TGTGTCATC TGCTTCAGTT
4401 CTTGAGGATA AAGTGTGAGC GACCAGCACA TTCTCACACC ACAAAGCCAC
4451 CTCATCTATT ACCACAGGGA CTCCTGAAAT CTCAACAAAG ACAAAGCCCA
4501 GCTCAGCCGT TCTTTCCTCC ATGACCCTAA GCAATGCAGC AACAAGTCCT
4551 GAAAGAGTCA GAAATGCAAC TTCCCCTCTG ACTCATCCAT CTCCATCAGG
4601 GGAAGAGACA GCAGGGAGTG TCCTCACTCT CAGCACCTCT GCTGAGACTA
4651 CAGACTCACC TAACATCCAC CCAACTGGGA CACTGACTTC AGAATCGTCA
4701 GAGAGTCCTA GCACTCTCAG CCTCCCAAGT GTCTCTGGAG TCAAACCAC
4751 ATTTTCTTCA TCTACTCCTT CCACTCATCT ATTTACTAGT GGAGAAGAAA
4801 CAGAGGAAAC TTCGAATCCA TCTGTGTCTC AACCTGAGAC TTCTGTTTCC
4851 AGAGTAAGGA CCACCTTGGC CAGCACCTCT GTCCCTACCC CAGTATTCCC
4901 CACCATGGAC ACCTGGCCTA CAGGTTGAGC TCAGTTCTCT TCATCCCACC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

4951 TAGTGAGTGA GCTCAGAGCT ACGAGCAGTA CCTCAGTTAC AAACCTCAACT
5001 GGTTCAGCTC TTCCTAAAAT ATCTCACCTC ACTGGGACGG CAACAATGTC
5051 ACAGACCAAT AGAGACACGT TTAATGACTC TGCTGCACCC CAAAGCACAA
5101 CTTGGCCAGA GACTAGTCCC AGATTCAAGA CAGGGTTACC TTCAGCAACA
5151 ACCACTGTTT CAACCTCTGC CACTTCTCTC TCTGCTACTG TAATGGTCTC
5201 TAAATTCACT TCTCCAGCAA CTAGTTCCAT GGAAGCAACT TCTATCAGGG
5251 AACCATCAAC AACCATCCTC ACAACAGAGA CCACGAATGG CCCAGGCTCT
5301 ATGGCTGTGG CTTCTACCAA CATCCCAATT GGAAAGGGCT ACATTACTGA
5351 AGGAAGATTG GACACAAGCC ATCTGCCCAT TGGAACCACA GCTTCCTCTG
5401 AGACATCTAT GGATTTTACC ATGGCCAAAG AAAGTGTCTC AATGTCAGTA
5451 TCTCCATCTC AGTCCATGGA TGCTGCTGGC TCAAGCACTC CAGGAAGGAC
5501 AAGCCAATTC GTTGACACAT TTTCTGATGA TGTCTATCAT TTAACATCCA
5551 GAGAAATTAC AATACCTAGA GATGGAACAA GCTCAGCTCT GACTCCACAA
5601 ATGACTGCAA CTCACCCTCC ATCTCCTGAT CCTGGCTCTG CTAGAAGCAC
5651 CTGGCTTGGC ATCTTGTCCT CATCTCCTTC TTCTCCTACT CCCAAAGTCA
5701 CAATGAGCTC CACATTTTCA ACTCAGAGAG TCACCACAAG CATGATAATG
5751 GACACAGTTG AAAC TAGTCG GTGGAACATG CCCAACTTAC CTTCCACGAC
5801 TTCCTTGACA CCAAGTAATA TTCCAACAAG TGGTGCCATA GGAAAAAGCA
5851 CCCTGGTTCC CTTGGACACT CCATCTCCAG CCACATCATT GGAGGCATCA
5901 GAAGGGGGAC TTCCAACCCT CAGCACCTAC CCTGAATCAA CAAACACACC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

5951 CAGCATCCAC CTCGGAGCAC ACGCTAGTTC AGAAAGTCCA AGCACCATCA
6001 AACTTACCAT GGCTTCAGTA GTAAACCTG GCTCTTACAC ACCTCTCACC
6051 TTCCCCTCAA TAGAGACCCA CATTATGTA TCAACAGCCA GAATGGCTTA
6101 CTCTTCTGGG TCTTCACCTG AGATGACAGC TCCTGGAGAG ACTAACACTG
6151 GTAGTACCTG GGACCCACAC ACCTACATCA CCACTACGGA TCCTAAGGAT
6201 ACAAGTTCAG CTCAGGTCTC TACACCCAC TCAGTGAGGA CACTCAGAAC
6251 CACAGAAAAC CATCCAAAGA CAGAGTCCGC CACCCAGCT GCTTACTCTG
6301 GAAGTCCTAA AATCTCAAGT TCACCCAATC TCACCAGTCC GGCCACAAAA
6351 GCATGGACCA TCACAGACAC AACTGAACAC TCCACTCAAT TACATTACAC
6401 AAAATTGGCA GAAAAATCAT CTGGATTGTA GACACAGTCA GCTCCAGGAC
6451 CTGTCTCTGT AGTAATCCCT ACCTCCCCTA CCATTGGAAG CAGCACATTG
6501 GAACTAACTT CTGATGTCCC AGGGGAACCC CTGGTCCTTG CTCCCAGTGA
6551 GCAGACCACA ATCACTCTCC CCATGGCAAC ATGGCTGAGT ACCAGTTTGA
6601 CAGAGGAAAT GGCTTCAACA GACCTTGATA TTTCAAGTCC AAGTTCACCC
6651 ATGAGTACAT TTGCTATTTT TCCACCTATG TCCACACCTT CTCATGAACT
6701 TTCAAAGTCA GAGGCAGATA CCAGTGCCAT TAGAAATACA GATTCAACAA
6751 CGTTGGATCA GCACCTAGGA ATCAGGAGTT TGGGCAGAAC TGGGGACTTA
6801 ACAACTGTTC CTATCACCCC ACTGACAACC ACGTGGACCA GTGTGATTGA
6851 ACACTCAACA CAAGCACAGG ACACCCTTTC TGCAACGATG AGTCCTACTC
6901 ACGTGACACA GTCACTCAA GATCAAACAT CTATACCAGC CTCAGCATCC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

6951 CCTTCCCATC TTACTGAAGT CTACCCTGAG CTCGGGACAC AAGGGAGAAG
7001 CTCCTCTGAG GCAACCACTT TTTGGAAACC ATCTACAGAC ACACTGTCCA
7051 GAGAGATTGA GACTGGCCCA ACAAACATTC AATCCACTCC ACCCATGGAC
7101 AACACAACAA CAGGGAGCAG TAGTAGTGGA GTCACCCTGG GCATAGCCCA
7151 CCTTCCCATA GGAACATCCT CCCCAGCTGA GACATCCACA AACATGGCAC
7201 TGGAAAGAAG AAGTTCTACA GCCACTGTCT CTATGGCTGG GACAATGGGA
7251 CTCCTTGTTA CTAGTGCTCC AGGAAGAAGC ATCAGCCAGT CATTAGGAAG
7301 AGTTTCTCT GTCCTTTCTG AGTCAACTAC TGAAGGAGTC ACAGATTCTA
7351 GTAAGGGAAG CAGCCCAAGG CTGAACACAC AGGGAAATAC AGCTCTCTCC
7401 TCCTCTCTTG AACCCAGCTA TGCTGAAGGA AGCCAGATGA GCACAAGCAT
7451 CCCTCTAACC TCATCTCCTA CAACTCCTGA TGTGGAATTC ATAGGGGGCA
7501 GCACATTTTG GACCAAGGAG GTCACCACAG TTATGACCTC AGACATCTCC
7551 AAGTCTTCAG CAAGGACAGA GTCCAGCTCA GCTACCCTTA TGTCCACAGC
7601 TTTGGGAAGC ACTGAAAATA CAGGAAAAGA AAAACTCAGA ACTGCCTCTA
7651 TGGATCTTCC ATCTCCAAC CTATCAATGG AGGTGACACC ATGGATTTCT
7701 CTCACTCTCA GTAATGCCCC CAATACCACA GATTCACCTG ACCTCAGCCA
7751 TGGGGTGCAC ACCAGCTCTG CAGGGACTTT GGCCACTGAC AGGTCATTGA
7801 ATACTGGTGT CACTAGAGCC TCCAGATTGG AAAACGGCTC TGATACCTCT
7851 TCTAAGTCCC TGTCTATGGG AAACAGCACT CAACTTCCA TGACTTACAC
7901 AGAGAAGAGT GAAGTGTCTT CTTCAATCCA TCCCCGACCT GAGACCTCAG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

7951 CTCCTGGAGC AGAGACCACT TTGACTTCCA CTCCTGGAAA CAGGGCCATA
8001 AGCTTAACAT TGCCTTTTTC ATCCATTCCA GTGGAAGAAG TCATTTCTAC
8051 AGGCATAACC TCAGGACCAG ACATCAACTC AGCACCCATG ACACATTCTC
8101 CCATCACCCC ACCAACAATT GTATGGACCA GTACAGGCAC AATTGAACAG
8151 TCCACTCAAC CACTACATGC AGTTTCTTCA GAAAAAGTTT CTGTGCAGAC
8201 ACAGTCAACT CCATATGTCA ACTCTGTGGC AGTGTCTGCT TCCCCTACCC
8251 ATGAGAATTC AGTCTCTTCT GGAAGCAGCA CATCCTCTCC ATATTCCTCA
8301 GCCTCACTTG AATCCTTGGA TTCCACAATC AGTAGGAGGA ATGCAATCAC
8351 TTCCTGGCTA TGGGACCTCA CTACATCTCT CCCCACTACA ACTTGGCCAA
8401 GTACTAGTTT ATCTGAGGCA CTGTCCTCAG GCCATTCTGG GGTTCAAAC
8451 CCAAGTTCAA CTACGACTGA ATTTCCACTC TTTTCAGCTG CATCCACATC
8501 TGCTGCTAAG CAAAGAAATC CAGAAACAGA GACCCATGGT CCCCAGAATA
8551 CAGCCGCGAG TACTTTGAAC ACTGATGCAT CCTCGGTCAC AGGTCTTTCT
8601 GAGACTCCTG TGGGGGCAAG TATCAGCTCT GAAGTCCCTC TTCCAATGGC
8651 CATAACTTCT AGATCAGATG TTTCTGGCCT TACATCTGAG AGTACTGCTA
8701 ACCCGAGTTT AGGCACAGCC TCTTCAGCAG GGACCAAATT AACTAGGACA
8751 ATATCCCTGC CCACTTCAGA GTCTTTGGTT TCCTTTAGAA TGAACAAGGA
8801 TCCATGGACA GTGTCAATCC CTTTGGGGTC CCATCCAACCT ACTAATACAG
8851 AAACAAGCAT CCCAGTAAAC AGCGCAGGTC CACCTGGCTT GTCCACAGTA
8901 GCATCAGATG TAATTGACAC ACCTTCAGAT GGGGCTGAGA GTATTCACAC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

8951 TGTCTCCTTT TCCCCCTCCC CTGATACTGA AGTGACAACT ATCTCACATT
9001 TCCCAGAAAA GACAACTCAT TCATTTAGAA CCATTTCATC TCTCACTCAT
9051 GAGTTGACTT CAAGAGTGAC ACCTATTCCT GGGGATTGGA TGAGTTCAGC
9101 TATGTCTACA AAGCCCACAG GAGCCAGTCC CTCCATTACA CTGGGAGAGA
9151 GAAGGACAAT CACCTCTGCT GCTCCAACCA CTTCCCCCAT AGTTCTCACT
9201 GCTAGTTTCA CAGAGACCAG CACAGTTTCA CTGGATAATG AAACACAGT
9251 AAAAACCTCA GATATCCTTG ACGCACGGAA AACAAATGAG CTCCCCTCAG
9301 ATAGCAGTTC TTCTTCTGAT CTGATCAACA CCTCCATAGC TTCTTCAACT
9351 ATGGATGTCA CTAAACAGC CTCCATCAGT CCCACTAGCA TCTCAGGAAT
9401 GACAGCAAGT TCCTCCCCAT CTCTCTTCTC TTCAGATAGA CCCAGGTTC
9451 CCACATCTAC AACAGAGACA AATACAGCCA CCTCTCCATC TGTTTCCAGT
9501 AACACCTATT CTCTTGATGG GGGCTCCAAT GTGGGTGGCA CTCCATCCAC
9551 TTTACCACCC TTTACAATCA CCCACCCTGT CGAGACAAGC TCGGCCCTAT
9601 TAGCCTGGTC TAGACCAGTA AGAACTTTCA GCACCATGGT CAGCACTGAC
9651 ACTGCCTCCG GAGAAAATCC TACCTCTAGC AATTCTGTGG TGACTTCTGT
9701 TCCAGCACCA GGTACATGGA CCAGTGTAGG CAGTACTACT GACTTACCTG
9751 CCATGGGCTT TCTCAAGACA AGTCCTGCAG GAGAGGCACA CTCACCTCTA
9801 GCATCAACTA TTGAACCAGC CACTGCCTTC ACTCCCCATC TCTCAGCAGC
9851 AGTGGTCACT GGATCCAGTG CTACATCAGA AGCCAGTCTT CTCACCTACGA
9901 GTGAAAGCAA AGCCATTCAT TCTTCACCAC AGACCCCAAC TACACCCACC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

9951 TCTGGAGCAA ACTGGGAAAC TTCAGCTACT CCTGAGAGCC TTTTGGTAGT
10001 CACTGAGACT TCAGACACAA CACTTACCTC AAAGATTTTG GTCACAGATA
10051 CCATCTTGTT TTCAACTGTG TCCACGCCAC CTTCTAAATT TCCAAGTACG
10101 GGGACTCTGT CTGGAGCTTC CTTCCCTACT TTA CTCCCGG ACACTCCAGC
10151 CATCCCTCTC ACTGCCACTG AGCCAACAAG TTCATTAGCT ACATCCTTTG
10201 ATTCCACCCC ACTGGTGACT ATAGCTTCGG ATAGTCTTGG CACAGTCCCA
10251 GAGACTACCC TGACCATGTC AGAGACCTCA AATGGTGATG CACTGGTTCT
10301 TAAGACAGTA AGTAACCCAG ATAGGAGCAT CCCTGGAATC ACTATCCAAG
10351 GAGTAACAGA AAGTCCACTC CATCCTTCTT CCACTTCCCC CTCTAAGATT
10401 GTTGCTCCAC GGAATACAAC CTATGAAGGT TCGATCACAG TGGCACTTTC
10451 TACTTTGCCT GCGGGAATA CTGGTTCCCT TGTATTCACT CAGAGTTCTG
10501 AAAACTCAGA GACAACGGCT TTGGTAGACT ATCAGCIGG GCTTGAGAGG
10551 GCATCTGTGA TGCCACTAAC CACAGGAAGC CAGGGTATGG CTAGCTCTGG
10601 AGGAATCAGA AGTGGGTCCA CTCCTCAAC TGGAACCAAA ACATTTTCTT
10651 CTCTCCCTCT GACCATGAAC CCAGGTGAGG TTACAGCCAT GTCTGAAATC
10701 ACCACGAACA GACTGACAGC TACTCAATCA ACAGCACCCA AAGGGATACC
10751 TGTGAAGCCC ACCAGTGCTG AGTCAGGCCT CCTAACACCT GTCTCTGCCT
10801 CCTCAAGCCC ATCAAAGGCC TTTGCCTCAC TGA CTACAGC TCCCCAACT
10851 TGGGGGATCC CACAGTCTAC CTTGACATTG GAGTTTCTG AGGTCCCAAG
10901 TTTGGATACT AAGTCCGCTT CTTTACCAAC TCCTGGACAG TCCCTGAACA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

10951 CCATTCCAGA CTCAGATGCA AGCACAGCAT CTCCTCACT GTCCAAGTCT
 11001 CCAGAAAAAA ACCCAAGGGC AAGGATGATG ACTTCCACAA AGGCCATAAG
 11051 TGCAAGCTCA TTTCAATCAA CAGGTTTTAC TGAAACCCCT GAGGGATCTG
 11101 CCTCCCCTTC TATGGCAGGG CATGAACCCA GAGTCCCAC TTCAGGAACA
 11151 GGGGACCCTA GATATGCCTC AGAGAGCATG TCTTATCCAG ACCCAAGCAA
 11201 GGCATCATCA GCTATGACAT CGACCTCTCT TGCATCAAAA CTCACAATC
 11251 TCTTCAGCAC AGGTCAAGCA GCAAGGTCTG GTTCTAGTTC CTCTCCCATA
 11301 AGCCTATCCA CTGAGAAAGA AACAAGCTTC CTTTCCCCCA CTGCATCCAC
 11351 CTCCAGAAAG ACTTCACTAT TTCTTGGGCC TTCCATGGCA AGGCAGCCCA

[0054] 11401 ACATATTGGT GCATCTTCAG ACTTCAGCTC TGACACTTTC
 TCCAACATCC

11451 ACTCTAAATA TGTCCCAGGA GGAGCCTCCT GAGTTAACCT CAAGCCAGAC
 11501 CATTGCAGAA GAAGAGGGAA CAACAGCTGA AACACAGACG TTAACCTTCA
 11551 CACCATCTGA GACCCCAACA TCCTTGTTAC CTGTCTCTTC TCCCACAGAA
 11601 CCCACAGCCA GAAGAAAGAG TTCTCCAGAA ACATGGGCAA GCTCTATTTT
 11651 AGTTCCTGCC AAGACCTCCT TGGTTGAAAG TAAGAATGCC CTGCTCCTTC
 11701 CCCAAGTGTG CTGGGGATGA ATCTGGAAAT AACTACATC TTTTTTATTT
 11751 TTTAAACTTT TATATTTGAA AATATAAATA TTTTAGGTTC AGGGAACATG
 11801 TGCAGGTTTG TTATATAGGT AAATTGCATG TCATGGGGGC TTGGGGTACA
 11851 GATTACATCA TCAGCCAGGT AATAAGCCTA GTACCTGATC AGTAGATTTT
 11901 TTTTAATCCT CTCCCTCCTC CCAGCCTCCA CCCTCAATTC ACATGTCTCC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
11951	ATGTGTACTC	AAGGTTTAAT	TCCCACTTAT	GAGTGAGAAC	ATGCGGTATT
12001	TGTAAACTAC	ATCTTTATTT	TTGCTAACCT	CGAACTGAAA	TTTAGCATTT
12051	GTTTTATTGA	TGAATAGAGG	TAACAAAACA	AACCACATTA	ATCCTAGCAG
12101	TGCCTGTGCC	TTTGCCAACA	ACAGAAATTC	CGGACACTTT	CATATCCTAT
12151	GACAATTGTT	GCAAGCACTT	TTAAAAATCA	TGTACGACTT	TATTCATAAT
12201	TATAGTGGTT	ATTAGGCTTT	TCAATAGATC	TTATTTAATG	AGTTAGTAAA
12251	ATAAGTGCCT	GTATTATTGT	ATTACATTTG	TTTATTAAGA	TCTTGATAAC
12301	AACATTTCAA	TATAATCATT	TCCTTTGTTT	TTTAAATTTT	AGATTCAGGG
12351	GTATATGTGC	AGGTTTGTTA	CGTGGATATA	CTGCATAATG	ATGAGGTTTG
12401	GCTTCTAGTG	AACCCATCAG	CCAAATAGTG	AATGTTGTGC	CCAATAAGTA
12451	GTTTTTCAAT	CCTCACTTCA	CTCCCAGCCT	CCTCTATTTT	GGAGTCCCAG
12501	TGTCTATTAT	TTCTATCTTT	ATGTCCACAT	GTACCCATTG	GTTAGCTCCC
12551	ACTTATAAGT	GAGAATGTGC	AGTATTTAAT	TTTCTGTTTT	TGAGTTATTT
12601	TGCTTAGGTT	GATGGCCTTC	AGCTCCAGCC	ACGTTGCTTT	AAAGAACATG
12651	ATTTCAATTCT	TTTTTATGGC	TGCATAGTAC	TCCGAGGTGT	ATGTGTACCA
12701	GATTTTCTTT	ATCCACAATG	ATTCCTTTG	TAATCTAATA	TTTTATATTG
12751	TTATTTTATG	TTTTATTCTA	TATTTTATT	TTAATTTATA	AAGGAATTCA
12801	TATGGTTCAC	AAGCCTGTCA	AAGGGACCTA	TAATAAAAAG	AGGTTAAGAA
12851	TCCATGCTCT	AAACAGAATA	TTACTCCATT	TTATTTTCATT	TATTTTTTAA
12901	GAGACAGTCT	CACTCTGTCA	TCCAGGCTGG	AGTACAGTGG	AGTGATCATA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

12951 GCTCATTGCA ACCCTGAACT CTTGGGCACA AGCAATTCTC CTGCTTCATC
 13001 CTCCAGAGGA GCTGGGACTA CAGGTGCACA TCACCATGCC CAGCTAGTTT
 13051 TAAAAATTAT TTTGTAGAGA TGGTGTCTCA CTATCCTACC CAGGCTGGTC
 13101 TCAAACCTCCT GGGCTCAGGC AATCCTCCCA CTTTGACCTC CCAAAGTGTT
 13151 GAGATTACAG GGGCAAGCCA CTGTGCCTGG CCACTTGTC AATTTTAATT
 13201 TGTGATTACT TATAAAATGA ACCCCTTCCC ATCTGAGATC TGTCAGTCTT
 13251 TCTGGTQACG GTGCCTGGTG TCTGCTTTCT ACCATGTCCT GTTAGACTAG
 13301 TGTTTGATGG GAGGTCACCT GGGCAGCTGT CCAGCTCACT CACTGGGCTC
 13351 TAGAGCCTCT GAGTTGAAGC AAAATAGAAA GATCAGTCAA TGTAAGAAA
 13401 GCTCAAAAAC TGACATTCTG AAGTAATGGA TAGCTAAACC TTCCTATTGC

Exon 2

13451 CCTTTTCTTT CAGCAACTGA TGGAACGCTA GTGACCACCA TAAAGATGTC
 13501 AAGCCAGGCA GCACAAGGAA ATTCCACGTG GCCTGCCCCA GCAGAGGAGA
 13551 CGGGGACCAG TCCAGCAGGT AAATATAGAC CTTGTTTCCA TTTCTGCTCT
 13601 GCTAATGCCA CCCAAGCCTT TCTTTTCTTT TCTTTTCTTT TCTTTTCTTT
 13651 TCTTTTCTTT TCTTTTCTTT CTCTCCCTTT CTTTCTTTCT TTCTTTCTTT
 13701 CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT CTTTCTTTCT TTCTTTCTTT
 13751 CTTTCTTTCT TTCTTTCTTT CTTTCTTTCT CTTTCTTTCT TCTTTCTCTC
 13801 TCTCTCTTTC TTTCTTTCTC TTGTTCTTTT TAAATTTTTT ATTTTTTTAC
 13851 TTAATTTTTT TCACCCAAGC CTTAAGGCCA GTTTGGACCA GATAGTGAGA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
13901	CCCCACCTCT	ATAAAAAAAAA	TTTTTAAAAA	AAAAATAAGT	TGGGCATCGT
13951	GCAGGCCTGT	AGTCCCTGCT	ACTCGAGAGG	CCAAGGTGGG	AGGACAGCTT
14001	GCTGCTGACT	AAAAGTGCTG	CTTATTGATT	CTGGGAAGAA	AAAATATACA
14051	AGGCTTCAGT	TTCATTATTT	TATAAGTAAA	TGCTAGCAAC	TTTTCCTTTT
14101	TTTCTCTCTT	TCTCTCTTCC	TCTCTTTCTC	TCCTCTCCTT	CTCTTCTCTC
14151	TCTCTCTCTC	TCTCTCTCTC	TTTCTCTCTC	CTCTCCTTCT	CTTCTCTTCT
14201	TTCTCTCTCT	CTCTCTTTCA	TTTATTTTGT	AGACATGGTC	TCATTCTGTC
14251	ACCCAGGCTG	GAGTACAGTG	GTGTATATTT	ACTGCAGTAC	TCACTGTACT
14301	CACTGCAGCC	TCAAATTCCT	GGGCTCAAGC	TATCCTCTCA	CCTCAGCCTC
14351	CTGAGTAGCT	GGGCAGCAGT	CCAGCTCACT	CACTGGGCTC	TAGAGCCTCT
14401	GTGCTATGCC	CAGCTTATTG	TTGTTGTTTT	TTTAAATTTT	TTTTTTTGTA
14451	CAGATGGGGT	CTCACTATGT	GGCCCAAGGT	GGTCTTAAAC	TCCTGGCTCC
14501	AAGAGATCCT	CCCACCTCAG	CCTCCCAAAG	TGCAGGGATT	ACAGGTGTGA
14551	GCCACTGTGC	CCAGCCTAGA	CAGCATTTTT	TTTTTTTGAA	ACAGGGTCTC
14601	CCTCTGTTGC	CCAGGCTGGA	GTGCAATGGC	GTGTTTATGG	TTCCTGCAG
14651	CCTCAGCCTC	CTCAGTCTCA	AGCAATCCTC	CAACTTCAGC	CTCCCCAAC
14701	AGCTAGAACT	GCAGGTGATC	ATCACCAATT	AGCCTGGTTA	ATTGTGTGTG
14751	TATTTCTTAA	ATTTTTTGTA	GAGATAGTTC	TCACTATATT	GCTTGGGCTG
14801	GTCTCAAAC	CCTGGACTCA	AGTGATTCAC	CTACCTCGGC	CTCCCTAAGC
14851	ACTGGGATTA	CAGGCTTGAG	CCACCACACC	CGGCAAGGAC	TAGGTTTTAA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence	
(SEQ ID NO: 1)	

14901	AATAGGTTCC TAGGCTGGGT GTGGTGGCTT ACGCCCGTAA TCCCAGCACT
14951	TTGGGAGGCT GAGGTGGGCG GATCACGAGG TCAGGAGTTT GAGACCAGCC
15001	TGGCCAACAT AGTGAAACCC TGTCTCTACT AAAAATACAA AAAATTAGCT
15051	GGGCATAGTG GCACACACCT GTAATCCCAG CTACTCGGGA GGCTGAGGAA
15101	GGAGAATCAC TTGAACCTGG GAGGCGGAGG TTGCAGTGAG CCGAGATCAT
15151	GCCATTGCTC TCCAGCCTGG GTGACAGAGC AAGACTCCAT CTAAAAAAAA
15201	AAAAAAAAAGT TCCTTTGACT TCTTGACACT CTTCTCTGAG GATATTGATC
15251	ATTTTTCCTC AATAGATGTT ACTAATTGAA CACTTCTGTT GCTTCAACTT
15301	ACTAATTTAC ATGATCAATA GCCAATTAAT TCAGCAGGAG AGAATGCTAC
15351	AGAGTCGATT CTTTCTGTAC TTTCTTCTGC TCCAGAGTGA AGGATCTTTC
15401	TAAATCAGAG ACCATCACTG TGTTACACAGG GAGGGCCTAG GTGAACCTGA
15451	GATGGCAAAT GTTGCGTTTG TTCTACGGAA GAAGGGATTA TGGGTTGAAG
15501	TCCTTGGCAG TGCCAAATTG CTTAGAAAAA TGTGAAATAT GGTCCCTAGG
15551	AGTGCTCTTG GGATGTCACA TTTTCTCAC TCCTTTGACA GGTAGATGTT
15601	ATTTTCCTGA AGGCCAGGGA AAGGATTCAG AGGGAGGAAT GAATTTGAAA
15651	GAAATGAAG GTGACGAGAA AGAATGAGCT CATCTCCCTT ATCCTCTTTC
15701	TTCTCAAATC CTTAAGTAGC TTTGCAGTGA ACTAAGATTT GGGGGAACCT
15751	AGAGGAGGCT GAAAGTTGGA AGCTGAAATT GGCTTAGCAA GGGCAAGCTC
15801	CAAAGACAAA AGTGGAATA GTTTGGGGGT AGCCTTTTGC ATGGGTGAAA
15851	TCCTGGTTCA TCACATCCTC CTTATGCAA AGAGCCCTTT TATATGGGGC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

15901 ATGGGGAAAA ACTGAGCTAA AGGTGATAAT TTCTCCTGAG CAAGCCAGAT
15951 GGTCAAAGCT CTAAC TTCAC CATCTCCCTT GGAATGTTTA ATGTGTTCCC
16001 TGGTGTCCAG AGGCTTAACG TGTGAGAATT AAAAGCTCAA CATTCTCTTT
16051 CCCAGGGAAG GAGGAAATAG TTTTAATTGA AATCCCGGGA GGAAATGAAT
16101 GATAGTGTCA AACCAAAAAA CTTTCATCTTC TGTACCACTT GCATATACTC

Exon 3

16151 CACTGACTTA CTTTCTAATC ACAGGCACAT CCCCAGGAAG CCCAGAAATG
16201 TCTACCACTC TCAAAATCAT GAGCTCCAAG GAACCCGGCA TCAGCCCAGA
16251 GATCAGGTCC ACTGTGAGAA ATTCTCCTTG GAAGACTCCA GAAACAACTG
16301 TTCCCATGGA GACCACAGTG GAACCAGTCA CCCTTCAGTC CACAGCCCTA
16351 GGAAGTGGCA GCACCAGCAT CTCTCACCTG CCCACAGGAA CCACATCACC
16401 AACCAAGTCA CCAACAGAAA ATATGTTGGC TACAGAAAGG GTCTCCCTCT
16451 CCCCATCCCC ACCTGAGGCT TGGACCAACC TTTATTCTGG AACTCCAGGA
16501 GGGACCAGGC AGTCACTGGC CACAATGTCC TCTGTCTCCC TAGAGTCACC
16551 AACTGCTAGA AGCATCACAG GGA CTGGTCA GCAAAGCAGT CCAGAACTGG
16601 TTTTAAAGAC AACTGGAATG GAATTCTCTA TGTGGCATGG CTCTACTGGA
16651 GGGACCACAG GGGACACACA TGTCTCTCTG AGCACATCTT CCAATATCCT
16701 TGAAGACCCT GTAACCAGCC CAACTCTGT GAGCTCATTG ACAGATAAAT
16751 CCAAACATAA AACCGAGACA TGGGTCAGCA CCACAGCCAT TCCCTCCACT
16801 GTCCTGAATA ATAAGATAAT GGCAGCTGAA CAACAGACAA GTCGATCTGT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
16851	<u>GGATGAGGCT TATTCATCAA CTAGTTCTTG GTCAGATCAG ACATCTGGGA</u>
16901	<u>GTGACATCAC CCTTGGTGCA TCTCCTGATG TCACAAACAC ATTATACATC</u>
16951	<u>ACCTCCACAG CACAAACCAC CTCACTAGTA TCTCTGCCCT CTGGAGACCA</u>
17001	<u>AGGCATTACA AGCCTCACCA ATCCCTCAGG AGGAAAAACA AGCTCTGCAT</u>
17051	<u>CATCTGTCAC ATCTCCTTCA ATAGGGCTTG AGACTCTGAT GGCCAATGTA</u>
17101	<u>AGTGCACTGA CAAGTGACAT TGCCCCTACT GCTGGGCATC TATCTCAGAC</u>
17151	<u>TTCATCTCCT GCGGAAGTGA GCATCCTGGA CATAACCACA GCTCCTACTC</u>
17201	<u>CAGGTATCTC CACCACCATC ACCACCATGG GAACCAACTC AATCTCAACT</u>
17251	<u>ACCACACCCA ACCCAGAAGT GGGTATGAGT ACCATGGACA GCACCCCGGC</u>
17301	<u>CACAGAGAGG CACACAACTT CTACAGAACA CCCTTCCACC TGGTCTTCCA</u>
17351	<u>CAGCTGCATC AGATTCTTGG ACTGTCACAG ACATGACTTC AAAGTTGAAA</u>
17401	<u>GTTGCAAGAT CTCCTGGAAC AATTTCACCA ATGCATACAA CTTCATTCTT</u>
17451	<u>AGCCTCAAGC ACTGAATTAG ACTCCATGTC TACTCCCCAT GGCCGTATAA</u>
17501	<u>CTGTCATTGG AACCAGCCTG GTCACTCCAT CCTCTGATGC TTCAGCTGTA</u>
17551	<u>AAGACAGAGA CCAGTACAAG TGAAAGAACA TTGAGTCCTT CAGACACAAC</u>
17601	<u>TGCATCTACT CCCATCTCAA CTTTTTCTCG TGTCCAGAGG ATGAGCATCT</u>
17651	<u>CAGTTCCTGA CATTTTAAGT ACAAGTTGGA CTCCCAGTAG TACAGAAGCA</u>
17701	<u>GAAGATGTGC CTGTTTCAAT GGTTCCTACA GATCATGCTA GTACAAAGAC</u>
17751	<u>TGACCCAAAT ATGCCCTGT CCACTTTTCT GTTTGATTCT CTGTCCACTC</u>
17801	<u>TTGACTGGGA CACTGGGAGA TCTCTGTCAT CAGCCACAGC CACTACCTCA</u>

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
17851	<u>GCTCCTCAGG GGGCCACAAC TCCCCAAGAA CTCACTTTGG AAACCATGAT</u>
17901	<u>CAGCCCAGCT ACCTCACAGT TGCCCTTCTC TATAGGGCAC ATTACAAGTG</u>
17951	<u>CAGTCATACC AGCTGCAATG GCAAGGAGCT CTGGAGTTAC TTTTCAAGA</u>
18001	<u>CCAGATCCCA CAAGCAAAAA GGCAGAGCAG ACTTCCACTC AGCTTCCCAC</u>
18051	<u>CACCACTTCT GCACATCCAG AGCAGGTGCC CAGATCAGCA GCAACAATC</u>
18101	<u>TGGATGTGAT CCCACACACA GCAAAAACTC CAGATGCAAC TTTTCAGAGA</u>
18151	<u>CAAGGGCAGA CAGCTCTTAC AACAGAGGCA AGAGCTACAT CTGACTCCTG</u>
18201	<u>GAATGAGAAA GAAAAATCAA CCCCAAGTGC ACCTTGGATC ACTGAGATGA</u>
18251	<u>TGAATTCTGT CTCAGAAGAT ACCATCAAGG AGGTACCAG CTCCTCCAGT</u>
18301	<u>GTGTTAAGGA CCCTGAATAC GCTGGACATA AACTTGGAAT CTGGGACGAC</u>
18351	<u>TCATCCCCA AGTTGGAAAA GCAGCCCATA TGAGAGAATT GCCCCTTCTG</u>
18401	<u>AGTCTACCAC AGACAAAGAG GCAATTCACC (TCTAC/AA CACAGTAGAG</u>
18451	<u>ACCACTGGCT GGGTCACAAG TTCCGAACAT GCTTCTCATT CCACTATCCC</u>
18501	<u>AGCCCACTCA GCGTCATCCA AACTCACATC TCCAGTGGTT ACAACCTCCA</u>
18551	<u>CCAGGGAACA AGCAATAGTT TCTATGTCAA CAACCACATG GCCAGAGTCT</u>
18601	<u>ACAAGGGCTA GAACAGAGCC TAATTCCTTC TTGACTATTG AACTGAGGGA</u>
18651	<u>CGTCAGCCCT TACATGGACA CCAGCTCAAC CACACAAACA AGTTTTATCT</u>
18701	<u>CTTCCCCAGG TTCCACTGCG ATCACCAAGG GGCCTAGAAC AGAAATTACC</u>
18751	<u>TCCTCTAAGA GAATATCCAG CTCATTCCTT GCCCAGTCTA TGAGGTCGTC</u>
18801	<u>AGACAGCCCC TCAGAAGCCA TCTCCAGGCT GTCTAACTTT CCTGCCATGA</u>

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

18851 CAGAATCTGG AGGAATGATC CTTGCTATGC AAACAAGTCC ACCTGGCGCT
18901 ACATCACTAA GTGCACCTAC TTTGGATACA TCAGCCACAG CCTCCTGGAC
18951 AGGGACTCCA CTGGCTACGA CTCAGAGATT TACATACTCA GAGAAGACCA
19001 CTCTCTTTAG CAAAGGTCCT GAGGATACAT CACAGCCAAG CCCTCCCTCT
19051 GTGGAAGAAA CCAGCTCTTC CTCTTCCCTG GTACCTATCA ATGCTACAAC
19101 CTCGCCTTCC AATATTTTGT TGACATCACA AGGGCACAGT CCCTCCTCTA
19151 CTCCACCTGT GACCTCAGTT TTCTTGTCTG AGACCTCTGG CCTGGGGAAG
19201 ACCACAGACA TGTCGAGGAT AAGCTTGGA CCTGGCACAA GTTTACCTCC
19251 CAATTTGAGC AGTACAGCAG GTGAGGCGTT ATCCACTTAT GAAGCCTCCA
19301 GAGATACAAA GGCAATTCAT CATTCTGCAG ACACAGCAGT GACGAATATG
19351 GAGGCAACCA GTTCTGAATA TTCTCCTATC CCAGGCCATA CAAAGCCATC
19401 CAAAGCCACA TCTCCATTGG TTACCTCCCA CATCATGGGG GACATCACTT
19451 CTTCCACATC AGTATTTGGC TCCTCCGAGA CCACAGAGAT TGAGACAGTG
19501 TCCTCTGTGA ACCAGGGACT TCAGGAGAGA AGCACATCCC AGGTGGCCAG
19551 CTCTGCTACA GAGACAAGCA CTGTCATTAC CCATGTGTCT AGTGGTGATG
19601 CTACTACTCA TGTCACCAAG ACACAAGCCA CTTTCTCTAG CGGAACATCC
19651 ATCTCAAGCC CTCATCAGTT TATAACTTCT ACCAACACAT TTACAGATGT
19701 GAGCACCAAC CCCTCCACCT CTCTGATAAT GACAGAATCT TCAGGAGTGA
19751 CCATCACCAC CCAAACAGGT CCTACTGGAG CTGCAACACA GGGTCCATAT
19801 CTCTTGGA CAATCAACCAT GCCTTACTTG ACAGAGACTC CATTAGCTGT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

19851 GACTCCAGAT TTTATGCAAT CAGAGAAGAC CACTCTCATA AGCAAAGGTC
19901 CCAAGGATGT GTCCTGGACA AGCCCTCCCT CTGTGGCAGA AACCAGCTAT
19951 CCCTCTTCCC TGACACCTTT CTTGGTCACA ACCATACCTC CTGCCACTTC
20001 CACGTTACAA GGGCAACATA CATCCTCTCC TGTTTCTGCG ACTTCAGTTC
20051 TTACCTCTGG ACTGGTGAAG ACCACAGATA TGTTGAACAC AAGCATGGAA
20101 CCTGTGACCA ATTCACCTCA AAATTGTAAC AATCCATCAA ATGAGATACT
20151 GGCCACTTTG GCAGCCACCA CAGATATAGA GACTATTCAT CCTTCCATAA
20201 ACAAAGCAGT GACCAATATG GGGACTGCCA GTTCAGCACA TGTACTGCAT
20251 TCCACTCTCC CAGTCAGCTC AGAACCATCT ACAGCCACAT CTCCAATGGT
20301 TCCTGCCTCC AGCATGGGGG ACGCTCTTGC TTCTATATCA ATACCTGGTT
20351 CTGAGACCAC AGACATTGAG GGAGAGCCAA CATCCTCCCT GACTGCTGGA
20401 CGAAAAGAGA ACAGCACCT CCAGGAGATG AACTCAACTA CAGAGTCAAA
20451 CATCATCCTC TCCAATGTGT CTGTGGGGGC TATTACTGAA GCCACAAAAA
20501 TGGAAGTCCC CTCTTTTGAT GCAACATTCA TACCAACTCC TGCTCAGTCA
20551 ACAAAGTTCC CAGATATTTT CTCAGTAGCC AGCAGTAGAC TTTCAAACCTC
20601 TCCTCCCATG ACAATATCTA CCCACATGAC CACCACCCAG ACAGGGTCTT
20651 CTGGAGCTAC ATCAAAGATT CCACTTGCCT TAGACACATC AACCTTGGA
20701 ACCTCAGCAG GGA CTCCATC AGTGGTGACT GAGGGGTTTG CCCACTCAA
20751 AATAACCACT GCAATGAACA ATGATGTCAA GGACGTGTCA CAGACAAACC
20801 CTCCCTTTCA GGATGAAGCC AGCTCTCCCT CTTCTCAAGC ACCTGTCCTT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
20851	<u>GTCACAACCT TACCTTCTTC TGTTGCTTTC ACACCGCAAT GGCACAGTAC</u>
20901	<u>CTCCTCTCCT GTTCTATGT CCTCAGTTCT TACTTCTTCA CTGGTAAAGA</u>
20951	<u>CCGCAGGCAA GGTGGATACA AGCTTAGAAA CAGTGACCAG TTCACCTCAA</u>
21051	<u>AGATATAGAG ACAACGCATC CTTCCATAAA CACAGTAGTT ACCAATGTGG</u>
21101	<u>GGACCACCGG TTCAGCATTT GAATCACATT CTACTGTCTC AGCTTACCCA</u>
21151	<u>GAGCCATCTA AAGTCACATC TCCAAATGTT ACCACCTCCA CCATGGAAGA</u>
21201	<u>CACCACAATT TCCAGATCAA TACCTAAATC CTCTAAGACT ACAAGAACTG</u>
21251	<u>AGACTGAGAC AACTTCCTCC CTGACTCCTA AACTGAGGGA GACCAGCGTC</u>
21301	<u>TCCCAGGAGA TCACCTCGTC CACAGAGACA AGCACTGTTC CTTACAAAGA</u>
21351	<u>GCTCACTGGT GCCACTACCG AGGTATCCAG GACAGATGTC ACTTCCTCTA</u>
21401	<u>GCAGTACATC CTTCCCTGGC CCTGATCAGT CCACAGTGTC ACTAGACATC</u>
21451	<u>TCCACAGAAA CCAACACCAG GCTGTCTACC TCCCCAATAA TGACAGAATC</u>
21501	<u>TGCAGAAATA ACCATCACCA CCCAAACAGG TCCTCATGGG GCTACATCAC</u>
21551	<u>AGGATACTTT TACCATGGAC CCATCAAATA CAACCCCCCA GGCAGGGATC</u>
21601	<u>CACTCAGCTA TGA CT CATGG ATTTTCACAA TTGGATGTGA CCACTCTTAT</u>
21651	<u>GAGCAGAATT CCACAGGATG TATCATGGAC AAGTCCTCCC TCTGTGGATA</u>
21701	<u>AAACCAGCTC CCCCTCTTCC TTTCTGCCCT CACCTGCAAT GACCACACCT</u>
21751	<u>TCCCTGATTT CTTCTACCTT ACCAGAGGAT AAGCTCTCCT CTCCTATGAC</u>
21801	<u>TTCACTTCTC ACCTCTGGCC TAGTGAAGAT TACAGACATA TTACGTACAC</u>
21851	<u>GCTTGGAACC TGTGACCAGC TCACTTCCAA ATTTCAGCAG CACCTCAGAT</u>

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
<hr/>	
21901	<u>AAGATACTGG CCACTTCTAA AGACAGTAAA GACACAAAGG AAATTTTTC</u>
21951	<u>TTCTATAAAC ACAGAAGAGA CCAATGTGAA AGCCAACAAC TCTGGACATG</u>
22001	<u>AATCCCATTG CCTGCACTG GCTGACTCAG AGACACCCAA AGCCACAAC</u>
22051	<u>CAAATGGTTA TCACCACCAC TGTGGGAGAT CCAGCTCCTT CCACATCAAT</u>
22101	<u>GCCAGTGCAT GGTTCCTCTG AGACTACAAA CATTAAGAGA GAGCCAACAT</u>
22151	<u>ATTTCTTGAC TCCTAGACTG AGAGAGACCA GTACCTCTCA GGAGTCCAGC</u>
22201	<u>TTTCCCACGG ACACAAGTTT TCTACTTTCC AAAGTCCCCA CTGGTACTAT</u>
22251	<u>TACTGAGGTC TCCAGTACAG GGGTCATCTC TTCTAGCAA ATTTCCACCC</u>
22301	<u>CAGACCATGA TAAGTCCACA GTGCCACCTG ACACCTTCAC AGGAGAGATC</u>
22351	<u>CCCAGGGTCT TCACCTCCTC TATTAAGACA AAATCTGCAG AAATGACGAT</u>
22401	<u>CACCACCCAA GCAAGTCCTC CTGAGTCTGC ATCGCACAGT ACCCTTCCCT</u>
22451	<u>TGGACACATC AACCACACTT TCCCAGGGAG GGACTCATT CACTGTGACT</u>
22501	<u>CAGGGATTCC CATACTCAGA GGTGACCACT CTCATGGGCA TGGGTCCTGG</u>
22551	<u>GAATGTGTCA TGGATGACAA CTCCCCCTGT GGAAGAAACC AGCTCTGTGT</u>
22601	<u>CTTCCCTGAT GTCTTCACCT GCCATGACAT CCCCTTCTCC TGTTCCTCC</u>
22651	<u>ACATCACCAC AGAGCATCCC CTCCTCTCCT CTTCTGTGA CTGCACTTCC</u>
22701	<u>TACTTCTGTT CTGGTGACAA CCACAGATGT GTTGGGCACA ACAAGCCCAG</u>
22751	<u>AGTCTGTAAC CAGTTCACCT CCAAATTGA GCAGCATCAC TCATGAGAGA</u>
22801	<u>CCGGCCACTT ACAAAGACAC TGCACACACA GAAGCCGCCA TGCATCATTC</u>
22851	<u>CACAAACACC GCAGTGACCA ATGTAGGGAC TTCCGGGTCT GGACATAAAT</u>

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

22901 CACAATCCTC TGTCTAGCT GACTCAGAGA CATCGAAAGC CACACCTCTG
22951 ATGAGTACCA CCTCCACCCT GGGGGACACA AGTGTTTCCA CATCAACTCC
23001 TAATATCTCT CAGACTAACC AAATTCAAAC AGAGCCAACA GCATCCCTGA
23051 GCCCTAGACT GAGGGAGAGC AGCACGTCTG AGAAGACCAG CTCAACAACA
23101 GAGACAAATA CTGCCTTTTC TTATGTGCCC ACAGGTGCTA TTA CT CAGGC
23151 CTCCAGAACA GAAATCTCCT CTAGCAGAAC ATCCATCTCA GACCTTGATC
23201 GGTCCACAAT AGCACCCGAC ATCTCCACAG GAATGATCAC CAGGCTCTTC
23251 ACCTCCCCCA TCATGACAAA ATCTGCAGAA ATGACCGTCA CCACTCAAAC
23301 AACTACTCCT GGGGCTACAT CACAGGGTAT CCTTCCCTGG GACACATCAA
23351 CCACACTTTT CCAGGGAGGG ACTCATTCAA CCGTGTCTCA GGGATTCCCA
23401 CACTCAGAGA TAACCACTCT TCGGAGCAGA ACCCCTGGAG ATGTGTCATG
23451 GATGACAACT CCCCCTGTGG AAGAAACCAG CTCTGGGTTT TCCCTGATGT
23501 CACCTTCCAT GACATCCCCT TCTCCTGTTT CCTCCACATC ACCAGAGAGC
23551 ATCCCCTCCT CTCCTCTCCC TGTGACTGCA CTTCTTACTT CTGTTCTGGT
23601 GACAACCACA AATGTATTGG GCACAACAAG CCCAGAGCCC GTAACGAGTT
23651 CACCTCCAAA TTTAAGCAGC CCCACACAGG AGAGACTGAC CACTTACAAA
23701 GACACTGCGC ACACAGAAGC CATGCATGCT TCCATGCATA CAAACACTGC
23751 AGTGGCCAAC GTGGGGACCT CCATTTCTGG ACATGAATCA CAATCTTCTG
23801 TCCCAGCTGA TTCAGACACA TCAAAGCCA CATCTCCAAT GGGTACCACC
23851 TTCGCCATGG GGGATACAAG TGTTTCTACA TCAACTCCTG CCTTCTTTGA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
23901	<u>GACTAGAATT CAGACTGAAT CAACATCCTC TTTGATTCTT GGATTAAGGG</u>
23951	<u>ACACCAGGAC GTCTGAGGAG ATCAACACTG TGACAGAGAC CAGCACTGTC</u>
24001	<u>CTTTCAGAAG TGCCCACTAC TACTACTACT GAGGTCTCCA GGACAGAAGT</u>
24051	<u>TATCACTTCC AGCAGAACAA CCATCTCAGG GCCTGATCAT TCCAAAATGT</u>
24101	<u>CACCCTACAT CTCCACAGAA ACCATCACCA GGCTCTCCAC TTTTCCTTTT</u>
24151	<u>GTAACAGGAT CCACAGAAAT GGCCATCACC AACCAAACAG GTCCTATAGG</u>
24201	<u>GACTATCTCA CAGGCTACCC TTACCCTGGA CACATCAAGC ACAGCTTCCT</u>
24251	<u>GGGAAGGGAC TCACTCACCT GTGACTCAGA GATTTCACA CTCAGAGGAG</u>
24301	<u>ACCACTACTA TGAGCAGAAG TACTAAGGGC GTGTCATGGC AAAGCCCTCC</u>
24351	<u>CTCTGTGGAA GAAACCAGTT CTCCTTCTTC CCCAGTGCCT TTACCTGCAA</u>
24401	<u>TAACCTCACA TTCATCTCTT TATTCCGAG TATCAGGAAG TAGCCCCACT</u>
24451	<u>TCTGCTCTCC CTGTGACTTC CTTTCTCACC TCTGGCAGGA GGAAGACCAT</u>
24501	<u>AGACATGTTG GACACACACT CAGAACTTGT GACCAGCTCC TTACCAAGTG</u>
24551	<u>CAAGTAGCTT CTCAGGTGAG ATACTCACTT CTGAAGCCTC CACAAATACA</u>
24601	<u>GAGACAATTC ACTTTTCAGA GAACACAGCA GAAACCAATA TGGGGACCAC</u>
24651	<u>CAATTCTATG CATAAACTAC ATTCTCTGT CTCAATCCAC TCCCAGCCAT</u>
24701	<u>CCGGACACAC ACCTCCAAAG GTTACTGGAT CTATGATGGA GGACGCTATT</u>
24751	<u>GTTTCCACAT CAACACCTGG TTCTCCTGAG ACTAAAAATG TTGACAGAGA</u>
24801	<u>CTCAACATCC CCTCTGACTC CTGAACTGAA AGAGGACAGC ACCGCCCTGG</u>
24851	<u>TGATGAACTC AACTACAGAG TCAAACACTG TTTTCTCCAG TGTGTCCCTG</u>

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

24901 GATGCTGCTA CTGAGGTCTC CAGGGCAGAA GTCACCTACT ATGATCCTAC
24951 ATTCATGCCA GCTTCTGCTC AGTCAACAAA GTCCCCAGAC ATTTACCTG
25001 AAGCCAGCAG CAGTCATTCT AACTCTCCTC CCTTGACAAT ATCTACACAC
25051 AAGACCATCG CCACACAAAC AGGTCTTCTT GGGGTGACAT CTCTTGGCCA
25101 ACTGACCCTG GACACATCAA CCATAGCCAC CTCAGCAGGA ACTCCATCAG
25151 CCAGAACTCA GGATTTTGTA GATTCAGAAA CAACCAGTGT CATGAACAAT
25201 GATCTCAATG ATGTGTTGAA GACAAGCCCT TTCTCTGCAG AAGAAGCCAA
25251 CTCTCTCTCT TCTCAGGCAC CTCTCCTTGT GACAACCTCA CCTTCTCCTG
25301 TAACTTCAC ATTGCAAGAG CACAGTACCT CCTCTCTTGT TTCTGTGACC
25351 TCAGTACCCA CCCCTACACT GCGAAGATC ACAGACATGG ACACAACTT
25401 AGAACCTGTG ACTCGTTCAC CTCAAATTT AAGGAACACC TTGGCCACTT
25451 CAGAAGCCAC CACAGATACA CACACAATGC ATCCTTCTAT AAACACAGCA
25501 GTGGCCAATG TGGGGACCAC CAGTTCACCA AATGAATTCT ATTTTACTGT
25551 CTCACCTGAC TCAGACCCAT ATAAAGCCAC ATCCGCAGTA GTTATCACTT
25601 CCACCTCGGG GGACTCAATA GTTCCACAT CAATGCCTAG ATCCTCTGCG
25651 ATGAAAAAGA TTGAGTCTGA GACAACTTTC TCCCTGATAT TTAGACTGAG
25701 GGAGACTAGC ACCTCCCAGA AAATTGGCTC ATCCTCAGAC ACAAGCACGG
25751 TCTTTGACAA AGCATTCACT GCTGCTACTA CTGAGGTCTC CAGAACAGAA
25801 CTCACCTCCT CTAGCAGAAC ATCCATCCAA GGCCTGAAA AGCCCACAAT
25851 GTCACCGGAC ACCTCCACAA GATCTGTCAC CATGCTTTCT ACTTTTGCTG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

25901 GCCTGACAAA ATCCGAAGAA AGGACCATTG CCACCCAAAC AGGTCCTCAT

25951 AGGGCGACAT CACAGGGTAC CCTTACCTGG GACACATCAA TCACAACCTC

26001 ACAGGCAGGG ACCCACTCAG CTATGACTCA TGGATTTTCA CAATTAGATT

26051 TGTCCACTCT TACGAGTAGA GTTCCTGAGT ACATATCAGG GACAAGCCCA

26101 CCCTCTGTGG AAAAAACCAG CTCTTCCTCT TCCCTTCTGT CTTTACCAGC

26151 AATAACCTCA CCGTCCCCTG TACCTACTAC ATTACCAGAA AGTAGGCCGT

26201 CTTCTCCTGT TCATCTGACT TCACTCCCCA CCTCTGGCCT AGTGAAGACC

26251 ACAGATATGC TGGCATCTGT GGCCAGTTTA CCTCCAAACT TGGGCAGCAC

26301 CTCACATAAG ATACCGACTA CTTCAGAAGA CATTAAAGAT ACAGAGAAAA

26351 TGTATCCTTC CACAAACATA GCAGTAACCA ATGTGGGGAC CACCACTTCT

26401 GAAAAGGAAT CTTATTCGTC TGTCCCAGCC TACTCAGAAC CACCCAAAGT

26451 CACCTCTCCA ATGGTTACCT CTTTCAACAT A TGGACACC ATTGTTTCCA

26501 CATCCATGCC TGGCTCCTCT GAGATTACAA GGATTGAGAT GGAGTCAACA

26551 TTCTCCCTGG CTCATGGGCT GAAGGGAACC AGCACCTCCC AGGACCCCAT

26601 CGTATCCACA GAGAAAAGTG CTGTCCTTCA CAAGTTGACC ACTGGTGCTA

26651 CTGAGACCTC TAGGACAGAA GTTGCCTCTT CTAGAAGAAC ATCCATTCCA

26701 GGCCCTGATC ATTCCACAGA GTCACCAGAC ATCTCCACTG AAGTGATCCC

26751 CAGCCTGCCT ATCTCCCTTG GCATTACAGA ATCTTCAAAT ATGACCATCA

26801 TCACTCGAAC AGGTCCTCCT CTTGGCTCTA CATCACAGGG CACATTTACC

26851 TTGGACACAC CAACTACATC CTCCAGGGCA GGAACACACT CGATGGCGAC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

26901 TCAGGAATTT CCACACTCAG AAATGACCAC TGTCATGAAC AAGGACCCTG
26951 AGATTCTATC ATGGACAATC CCTCCTTCTA TAGAGAAAAC CAGCTTCTCC
27001 TCTTCCCTGA TGCCTTCACC AGCCATGACT TCACCTCCTG TTTCTCAAC
27051 ATTACCAAAG ACCATTCA CACTCCTTC TCCTATGACC TCACTGCTCA
27101 CCCCTAGCCT AGTGATGACC ACAGACACAT TGGGCACAAG CCCAGAACCT
27151 ACAACCAGTT CACCTCCAAA TTTGAGCAGT ACCTCACATG AGATACTGAC
27201 AACAGATGAA GACACCACAG CTATAGAAGC CATGCATCCT TCCACAAGCA
27251 CAGCAGCGAC TAATGTGGAA ACCACCAGTT CTGGACATGG GTCACAATCC
27301 TCTGTCCTAG CTGACTCAGA AAAAACCAAG GCCACAGCTC CAATGGATAC
27351 CACCTCCACC ATGGGGCATA CAACTGTTTC CACATCAATG TCTGTTTCTT
27401 CTGAGACTAC AAAAATTAAG AGAGAGTCAA CATATTCCTT GACTCCTGGA
27451 CTGAGAGAGA CCAGCATTTC CCAAATGCC AGCTTTTCCA CTGACACAAG
27501 TATTGTTCTT TCAGAAGTCC CCACTGGTAC TACTGCTGAG GTCTCCAGGA
27551 CAGAAGTCAC CTCCTCTGGT AGAACATCCA TCCCTGGCCC TTCTCAGTCC
27601 ACAGTTTTGC CAGAAATATC CACAAGAACA ATGACAAGGC TCTTTGCCTC
27651 GCCCACCATG ACAGAATCAG CAGAAATGAC CATCCCCACT CAAACAGGTC
27701 CTTCTGGGTC TACCTCACAG GATACCCTTA CCTTGGACAC ATCCACCACA
27751 AAGTCCCAGG CAAAGACTCA TTCAACTTTG ACTCAGAGAT TTCCACACTC
27801 AGAGATGACC ACTCTCATGA GCAGAGGTCC TGGAGATATG TCATGGCAAA
27851 GCTCTCCCTC TCTGGAAAAT CCCAGCTCTC TCCCTTCCCT GCTGTCTTTA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

27901 CCTGCCACAA CCTCACCTCC TCCCATTTC TCCACATTAC CAGTGACTAT

27951 CTCCTCCTCT CCTCTTCCTG TGACTTCACT TCTCACCTCT AGCCCGGTAA

28001 CGACCACAGA CATGTTACAC ACAAGCCCAG AACTTGTAAC CAGTTCACCT

28051 CCAAAGCTGA GCCACACTTC AGATGAGAGA CTGACCACTG GCAAGGACAC

28101 CACAAATACA GAAGCTGTGC ATCCTTCCAC AAACACAGCA GCGTCCAATG

28151 TGGAGATTCC CAGCTCTGGA CATGAATCCC CTCCTCTGC CTTAGCTGAC

28201 TCAGAGACAT CCAAAGCCAC ATCACCAATG TTTATTACCT CCACCCAGGA

28251 GGATACAAC GTTGCCATAT CAACCCCTCA CTTCTTGGAG ACTAGCAGAA

28301 TTCAGAAAGA GTCAATTTCC TCCCTGAGCC CTAAATTGAG GGAGACAGGC

28351 AGTTCTGTGG AGACAAGCTC AGCCATAGAG ACAAGTGCTG TCCTTTCTGA

28401 AGTGTCCGTT GGTGCTACTA CTGAGATCTC CAGGACAGAA GTCACCTCCT

28451 CTAGCAGAAC ATCCATCTCT GGTTCGTCTG AGTCCACAAT GTTGCCAGAA

28501 ATATCCACCA CAAGAAAAAT CATTAAAGTTC CCTACTTCCC CCATCCTGGC

28551 AGAATCATCA GAAATGACCA TCAAGACCCA AACAAGTCCT CCTGGGTCTA

28601 CATCAGAGAG TACCTTTACA TTAGACACAT CAACCACTCC CTCCTTG GTA

28651 ATAACCCATT CGACTATGAC TCAGAGATTG CCACACTCAG AGATAACCAC

28701 TCTTGTGAGT AGAGGTGCTG GGGATGTGCC ACGGCCCAGC TCTCTCCCTG

28751 TGGAAGAAAC AAGCCCTCCA TCTTCCCAGC TGTCTTTATC TGCCATGATC

28801 TCACCTTCTC CTGTTTCTTC CACATTACCA GCAAGTAGCC ACTCCTCTTC

28851 TGCTTCTGTG ACTTCACTTC TCACACCAGG CCAAGTGAAG ACTACTGAGG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

28901 TGTTGGACGC AAGTGCAGAA CCTGAAACCA GTTCACCTCC AAGTTTGAGC

28951 AGCACCTCAG TTGAAATACT GGCCACCTCT GAAGTCACCA CAGATACGGA

29001 GAAAATTCAT CCTTTCTCAA ACACGGCAGT AACCAAAGTT GGAAGTTCCA

29051 GTTCTGGACA TGAATCCCCT TCCTCTGTCC TACCTGACTC AGAGACAACC

29101 AAAGCCACAT CGGCAATGGG TACCATCTCC ATTATGGGGG ATACAAGTGT

29151 TTCTACATTA ACTCCTGCCT TATCTAACAC TAGGAAAATT CAGTCAGAGC

29201 CAGCTTCCTC ACTGACCACC AGATTGAGGG AGACCAGCAC CTCTGAAGAG

29251 ACCAGCTTAG CCACAGAAGC AAACACTGTT CTTTCTAAAG TGTCCACTGG

29301 TGCTACTACT GAGGTCTCCA GGACAGAAGC CATCTCCTTT AGCAGAACAT

29351 CCATGTCAGG CCCTGAGCAG TCCACAATGT CACAAGACAT CTCCATAGGA

29401 ACCATCCCCA GGATTTCTGC CTCCTCTGTC CTGACAGAAT CTGCAAAAAT

29451 GACCATCACA ACCCAAACAG GTCCTTCGGA GTCTACACTA GAAAGTACCC

29501 TTAATTTGAA CACAGCAACC ACACCCTCTT GGGTGGAAC CCACTCTATA

29551 GTAATTCAGG GATTTCCACA CCCAGAGATG ACCACTTCCA TGGGCAGAGG

29601 TCCTGGAGGT GTGTCATGGC CTAGCCCTCC CTTTGTGAAA GAAACCAGCC

29651 CTCCATCCTC CCCGCTGTCT TTACCTGCCG TGACCTCACC TCATCCTGTT

29701 TCCACCACAT TCCTAGCACA TATCCCCCCC TCTCCCCCTC CTGTGACTTC

29751 ACTTCTCACC TCTGGCCCCG CGACAACCAC AGATATCTTG GGTACAAGCA

29801 CAGAACCTGG AACCAGTTCA TCTTCAAGTT TGAGCACCAC CTCCCATGAG

29851 AGACTGACCA CTTACAAAGA CACTGCACAT ACAGAAGCCG TGCATCCTTC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

29901 CACAAACACA GGAGGGACCA ATGTGGCAAC CACCAGCTCT GGATATAAAT
29951 CACAGTCCTC TGTCTAGCT GACTCATCTC CAATGTGTAC CACCTCCACC
30001 ATGGGGGATA CAAGTGTCT CACATCAACT CTGCCTTCC TTGAGACTAG
30051 GAGGATTCAG ACAGAGCTAG CTTCTCCCT GACCCCTGGA TTGAGGGAGT
30101 CCAGTGGCTC TGAAGGGACC AGCTCAGGCA CCAAGATGAG CACTGTCCTC
30151 TCTAAAGTGC CCACTGGTGC TACTACTGAG ATCTCCAAGG AAGACGTCAC
30201 CTCCATCCCA GGTCCCGCTC AATCCACAAT ATCACCAGAC ATCTCCACAA
30251 GAACCGTCAG CTGGTTCTCT ACATCCCCTG TCATGACAGA ATCAGCAGAA
30301 ATAACCATGA ACACCCATAC AAGTCCTTTA GGGGCCACAA CACAAGGCAC
30351 CAGTACTTTG GCCACGTCAA GCACAACCTC TTTGACAATG ACACACTCAA
30401 CTATATCTCA AGGATTTTCA CACTCACAGA TGAGCACTCT TATGAGGAGG
30451 GGTCCTGAGG ATGTATCATG GATGAGCCCT CCCCTTCTGG AAAAACTAG
30501 ACCTTCCTTT TCTCTGATGT CTTACCAGC CACAATTCA CCTTCTCCTG
30551 TTTCTCCAC ATTACCAGAG AGCATCTCTT CCTCTCCTCT TCCTGTGACT
30601 TCACTCCTCA CGTCTGGCTT GGCAAAAACCT ACAGATATGT TGCACAAAAG
30651 CTCAGAACCT GTAACCAACT CACCTGCAAA TTTGAGCAGC ACCTCAGTTG
30701 AAATACTGGC CACCTCTGAA GTCACCACAG ATACAGAGAA AACTCATCCT
30751 TCTTCAAACA GAACAGTGAC CGATGTGGGG ACCTCCAGTT CTGGACATGA
30801 ATCCACTTCC TTTGTCCTAG CTGACTCACA GACATCCAAA GTCACATCTC
30851 CAATGGTTAT TACCTCCACC ATGGAGGATA CGAGTGTCTC CACATCAACT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

30901 CCTGGCTTTT TTGAGACTAG CAGAATTCAG ACAGAACCAA CATCCTCCCT
30951 GACCCTTGGA CTGAGAAAGA CCAGCAGCTC TGAGGGGACC AGCTTAGCCA
31001 CAGAGATGAG CACTGTCCTT TCTGGAGTGC CCACTGGTGC CACTGCTGAA
31051 GTCTCCAGGA CAGAAGTCAC CTCCTCTAGC AGAACATCCA TCTCAGGCTT
31101 TGCTCAGCTC ACAGTGTAC CAGAGACTTC CACAGAAACC ATCACCAGAC
31151 TCCCTACCTC CAGCATAATG ACAGAATCAG CAGAAATGAT GATCAAGACA
31201 CAAACAGATC CTCCTGGGTC TACACCAGAG AGTACTCATA CTGTGGACAT
31251 ATCAACAACA CCCAACTGGG TAGAAACCCA CTCGACTGTG ACTCAGAGAT
31301 TTTCACACTC AGAGATGACC ACTCTTGTTA GCAGAAGCCC TGGTGATATG
31351 TTATGGCCTA GTCAATCCTC TGTGGAAGAA ACCAGCTCTG CCTCTTCCCT
31401 GCTGTCTCTG CCTGCCACGA CCTCACCTTC TCCTGTTTCC TCTACATTAG
31451 TAGAGGATTT CCCTTCCGCT TCTCTTCCTG TGACTTCTCT TCTCACCCTT
31501 GGCCTGGTGA TAACCACAGA CAGGATGGGC ATAAGCAGAG AACCTGGAAC
31551 CAGTTCCACT TCAAATTTGA GCAGCACCTC CCATGAGAGA CTGACCACTT
31601 TGGAAGACAC TGTAATATACA GAAGACATGC AGCCTTCCAC ACACACAGCA
31651 GTGACCAACG TGAGGACCTC CATTTCTGGA CATGAATCAC AATCTTCTGT
31701 CCTATCTGAC TCAGAGACAC CCAAAGCCAC ATCTCCAATG GGTACCACCT
31751 ACACCATGGG GGAAACGAGT GTTCCATAT CCACTTCTGA CTTCCTTGAG
31801 ACCAGCAGAA TTCAGATAGA ACCAACATCC TCCCTGACTT CTGGATTGAG
31851 GGAGACCAGC AGCTCTGAGA GGATCAGCTC AGCCACAGAG GGAAGCACTG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
<hr/>	
31901	<u>TCCTTTCTGA AGTGCCCACT GGTGCTACCA CTGAGGTCTC CAGGACAGAA</u>
31951	<u>GTGATATCCT CTAGGGGAAC ATCCATGTCA GGGCCTGATC AGTTCACCAT</u>
32001	<u>ATCACCAGAC ATCTCTACTG AAGCGATCAC CAGGCTTTCT ACTTCCCCCA</u>
32051	<u>TTATGACAGA ATCAGCAGAA AGTGCCATCA CTATTGAGAC AGGTTCTCCT</u>
32101	<u>GGGGCTACAT CAGAGGGTAC CCTCACCTTG GACACCTCAA CAACAACCTT</u>
32151	<u>TTGGTCAGGG ACCCACTCAA CTGCATCTCC AGGATTTTCA CACTCAGAGA</u>
32201	<u>TGACCACTCT TATGAGTAGA ACTCCTGGAG ATGTGCCATG GCCGAGCCTT</u>
32251	<u>CCCTCTGTGG AAGAAGCCAG CTCTGTCTCT TCCTCACTGT CTTACCTGC</u>
32301	<u>CATGACCTCA ACTTCTTTTT TCTCCACATT ACCAGAGAGC ATCTCCTCCT</u>
32351	<u>CTCCTCATCC TGTGACTGCA CTTCTACCC TTGGCCCAGT GAAGACCACA</u>
32401	<u>GACATGTTGC GCACAAGCTC AGAACCTGAA ACCAGTTCAC CTCCAAATTT</u>
32451	<u>GAGCAGCACC TCAGCTGAAA TATTAGCCAC GTCTGAAGTC ACCAAAGATA</u>
32501	<u>GAGAGAAAAT TCATCCCTCC TCAAACACAC CTGTAGTCAA TGTAGGGACT</u>
32551	<u>GTGATTTATA AACATCTATC CCCTTCCTCT GTTTTGGCTG ACTTAGTGAC</u>
32601	<u>AACAAAACCC ACATCTCCAA TGGCTACCAC CTCCACTCTG GGGAATACAA</u>
32651	<u>GTGTTTCCAC ATCAACTCCT GCCTTCCCAG AAACATATGAT GACACAGCCA</u>
32701	<u>ACTTCCTCCC TGAATTCTGG ATTAAGGGAG ATCAGTACCT CTCAAGAGAC</u>
32751	<u>CAGCTCAGCA ACAGAGAGAA GTGCTTCTCT TTCTGGAATG CCCACTGGTG</u>
32801	<u>CTACTACTAA GGTCTCCAGA ACAGAAGCCC TCTCCTTAGG CAGAACATCC</u>
32851	<u>ACCCCAAGTC CTGCTCAATC CACAATATCA CCAGAAATCT CCACGGAAAC</u>

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

32901 CATCACTAGA ATTTCTACTC CCCTCACCAC GACAGGATCA GCAGAAATGA

32951 CCATCACCCC CAAAACAGGT CATTCTGGGG CATCCTCACA AGGTACCTTT

33001 ACCTTGGACA CATCAAGCAG AGCCTCCTGG CCAGGAACTC ACTCAGCTGC

33051 AACTCACAGA TCTCCACACT CAGGGATGAC CACTCCTATG AGCAGAGGTC

33101 CTGAGGATGT GTCATGGCCA AGCCGCCCAT CAGTGGAAAA AACTAGCCCT

33151 CCATCTTCCC TGGTGTCTTT ATCTGCAGTA ACCTCACCTT CGCCACTTTA

33201 TTCCACACCA TCTGAGAGTA GCCACTCATC TCCTCTCCGG GTGACTTCTC

33251 TTTTCACCCC TGTCATGATG AAGACCACAG ACATGTTGGA CACAAGCTTG

33301 GAACCTGTGA CCACTTCACC TCCAGTATG AATATCACCT CAGATGAGAG

33351 TCTGGCCACT TCTAAAGCCA CCATGGAGAC AGAGGCAATT CAGCTTTCAG

[0056] 33401 AAAACACAGC TGTGACTCAG ATGGGCACCA TCAGCGCTAG
ACAAGAATTC

33451 TATTCCTCTT ATCCAGGCCT CCCAGAGCCA TCCAAAGTGA CATCTCCAGT

33501 GGTCACCTCT TCCACCATAA AAGACATTGT TTCTACAACC ATACCTGCTT

33551 CCTCTGAGAT AACAAGAATT GAGATGGAGT CAACATCCAC CCTGACCCCC

33601 ACACCAAGGG AGACCAGCAC CTCCCAGGAG ATCCACTCAG CCACAAAGCC

33651 AAGCACTGTT CTTACAAGG CACTCACTAG TGCCACGATT GAGGACTCCA

33701 TGACACAAGT CATGTCCTCT AGCAGAGGAC CTAGCCCTGA TCAGTCCACA

33751 ATGTCACAAG ACATATCCAG TGAAGTGATC ACCAGGCTCT CTACCTCCCC

33801 CATCAAGGCA GAATCTACAG AAATGACCAT TACCACCCAA ACAGGTTCTC

33851 CTGGGGCTAC ATCAAGGGGT ACCCTTACCT TGGACACTTC AACAACTTTT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

33901 ATGTCAGGGA CCCACTCAAC TGCATCTCAA GGATTTTCAC ACTCACAGAT

33951 GACCGCTCTT ATGAGTAGAA CTCCTGGAGA TGTGCCATGG CTAAGCCATC

34001 CCTCTGTGGA AGAAGCCAGC TCTGCCTCTT TCTCACTGTC TTCACCTGTC

34051 ATGACCTCAT CTTCTCCCGT TTCTTCCACA TTACCAGACA GCATCCACTC

34101 TTCTTCGCTT CCTGTGACAT CACTTCTCAC CTCAGGGCTG GTGAAGACCA

34151 CAGAGCTGTT GGGCACAAGC TCAGAACCTG AAACCAGTTC ACCCCCAAAT

34201 TTGAGCAGCA CCTCAGCTGA AATACTGGCC ACCACTGAAG TCACTACAGA

34251 TACAGAGAAA CTGGAGATGA CCAATGTGGT AACCTCAGGT TATACACATG

34301 AATCTCCTTC CTCTGTCCTA GCTGACTCAG TGACAACAAA GGCCACATCT

34351 TCAATGGGTA TCACCTACCC CACAGGAGAT ACAAATGTTC TCACATCAAC

34401 CCCTGCCTTC TCTGACACCN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

34451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NI NNNNNNNNNN NNNNNNNNNN

34501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNCGGAAA CCAAGTTTCT

Exon 4

34551 AACCAACCCC TCCTTTTTGA CCCCACTAGG ATTCAAACAA AGTCAAAGCT

34601 CTCACTGACT CCTGGGTTGA TGGAGACCAG CATCTCTGAA GAGACCAGCT

34651 CTGCCACAGA AAAAAGCACT GTCCTTTCTA GTGTGCCCAC TGGTGCTACT

34701 ACTGAGGTCT CCAGGACAGA AGCCATCTCT TCTAGCAGAA CATCCATCCC

34751 AGGCCCTGCT CAATCCACAA TGTCATCAGA CACCTCCATG GAAACCATCA

34801 CTAGAATTTC TACCCCCCTC ACAAGGAAAG AATCAACAGA CATGGCCATC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

34851 ACCCCCAAA CAGGTCCTTC TGGGGCTACC TCGCAGGGTA CCTTTACCTT
34901 GGACTCATCA AGCACAGCCT CCTGGCCAGG AACTCACTCA GCTACAACCTC
34951 AGAGATTTCC ACAGTCAGTG GTGACAACTC CTATGAGCAG AGGTCCTGAG
35001 GATGTGTCAT GGCCAAGCCC GCTGTCTGTG GAAAAAACA GCCCTCCATC
35051 TTCCCTGGTA TCTTCATCTT CAGTAACCTC ACCTTCGCCA CTTTATTCCA
35101 CACCATCTGG GAGTAGCCAC TCCTCTCCTG TCCCTGTCAC TTCTCTTTTC
35151 ACCTCTATCA TGATGAAGGC CACAGACATG TTGGATGCAA GTTTGGAACC
35201 TGAGACCACT TCAGCTCCCA ATATGAATAT CACCTCAGAT GAGAGTCTGG
35251 CCACTTCTAA AGCCACCACG GAGACAGAGG CAATTCACGT TTTTGAAAAT
35301 ACAGCAGCGT CCCATGTGGA AACCACCAGT GCTACAGAGG AACTCTATTC
35351 CTCTTCCCCA GGCTTCTCAG AGCCAACAAA AGTGATATCT CCAGTGGTCA
35401 CCTCTTCCTC TATAAGAGAC AACATGGTTT CCACAACAAT GCCTGGCTCC
35451 TCTGGCATT AAGGATTGA GATAGAGTCA ATGTCATCTC TGACCCCTGG
35501 ACTGAGGGAG ACCAGAACCT CCCAGGACAT CACCTCATCC ACAGAGACAA
35551 GCACTGTCCT TTACAAGATG TCCTCTGGTG CCACTCCTGA GGTCTCCAGG
35601 ACAGAAGTTA TGCCCTCTAG CAGAACATCC ATTCCTGGCC CTGCTCAGTC
35651 CACAATGTCA CTAGACATCT CCGATGAAGT TGTACCAGG CTGTCTACCT
35701 CTCCCATCAT GACAGAATCT GCAGAAATAA CCATCACCAC CCAAACAGGT
35751 TATTCTCTGG CTACATCCCA GGTTACCCCT CCCTTGGGCA CCTCAATGAC
35801 CTTTTTGTCA GGGACCCACT CAACTATGTC TCAAGGACTT TCACACTCAG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

35851 AGATGACCAA TCTTATGAGC AGGGGTCCTG AAAGTCTGTC ATGGACGAGC
35901 CCTCGCTTTG TGGAAACAAC TAGATCTTCC TCTTCTCTGA CATCATTACC
35951 TCTCACGACC TCACTTTCTC CTGTGTCCTC CACATTACTA GACAGTAGCC
36001 CCTCCTCTCC TCTTCCTGTG ACTTCACTTA TCCTCCCAGG CCTGGTGAAG
36051 ACTACAGAAG TGTTGGATAC AAGCTCAGAG CCTAAAACCA GTTCATCTCC
36101 AAATTTGAGC AGCACCTCAG TTGAAATACC GGCCACCTCT GAAATCATGA
36151 CAGATACAGA GAAAATTCAT CCTTCCTCAA ACACAGCGGT GGCCAAAGTG
36201 AGGACCTCCA GTTCTGTTCA TGAATCTCAT TCCTCTGTCC TAGCTGACTC
36251 AGAAACAACC ATAACCATAC CTTCAATGGG TATCACCTCC GCTGTGGACG
36301 ATACCACTGT TTTCACATCA AATCCTGCCT TCTCTGAGAC TAGGAGGATT
36351 CCGACAGAGC CAACATTCTC ATTGACTCCT GGATTGAGG AGACTAGCAC
36401 CTCTGAAGAG ACCACCTCAA TCACAGAAAC AAGTGCAGTC CTTTATGGAG
36451 TGCCCACTAG TGCTACTACT GAAGTCTCCA TGACAGAAAT CATGTCCTCT
36501 AATAGAACAC ACATCCCTGA CTCTGATCAG TCCACGATGT CTCCAGACAT
36551 CATCACTGAA GTGATCACCA GGCTCTCTTC CTCATCCATG ATGTCAGAAT
36601 CAACACAAAT GACCATCACC ACCCAAAAAA GTTCTCCTGG GGCTACAGCA
36651 CAGAGTACTC TTACCTTGGC CACAACAACA GCCCCCTTGG CAAGGACCCA
36701 CTCAACTGTT CCTCCTAGAT TTTTACACTC AGAGATGACA ACTCTTATGA
36751 GTAGGAGTCC TGAAAATCCA TCATGGAAGA GCTCTCCCTT TGTGGAAAAA
36801 ACTAGCTCTT CATCTTCTCT GTTGTCTTA CCTGTCACGA CCTCACCTTC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

36851 TGTTTCTTCC ACATTACCGC AGAGTATCCC TTCCTCCTCT TTTTCTGTGA
36901 CTTCACTCCT CACCCCAGGC ATGGTGAAGA CTACAGACAC AAGCACAGAA
36951 CCTGGAACCA GTTTATCTCC AAATCTGAGT GGCACCTCAG TTGAAATACT
37001 GGCTGCCTCT GAAGTCACCA CAGATACAGA GAAAATTCAT CCTTCTTCAA
37051 GCATGGCAGT GACCAATGTG GGAACCACCA GTTCTGGACA TGAATATAT
37101 TCCTCTGTTT CAATCCACTC GGAGCCATCC AAGGCTACAT ACCCAGTGGG
37151 TACTCCCTCT TCCATGGCTG AAACCTCTAT TTCCACATCA ATGCCTGCTA
37201 ATTTTGAGAC CACAGGATTT GAGGCTGAGC CATTTTCTCA TTTGACTTCT
37251 GGATTTAGGA AGACAAACAT GTCCCTGGAC ACCAGCTCAG TCACACCAAC
37301 AAATACACCT TCTTCTCCTG GGTCCACTCA CCTTTTACAG AGTTCCAAGA
37351 CTGATTTTAC CTCTTCTGCA AAAACATCAT CCCCAGACTG GCCTCCAGCC
37401 TCACAGTATA CTGAAATTCC AGTGGACATA ATCACCCCTT TTAATGCTTC
37451 TCCATCTATT ACGGAGTCCA CTGGGATAAC CTCCTTCCCA GAATCCAGGT
37501 TTACTATGTC TGTAACAGAA AGTACTCATC ATCTGAGTAC AGATTGCTG
37551 CCTTCAGCTG AGACTATTTT CACTGGCACA GTGATGCCTT CTCTATCAGA
37601 GGCCATGACT TCATTTGCCA CCACTGGAGT TCCACGAGCC ATCTCAGGTT
37651 CAGGTAGTCC ATTCTCTAGG ACAGAGTCAG GCCCTGGGGA TGCTACTCTG
37701 TCCACCATTG CAGAGAGCCT GCCTTCATCC ACTCCTGTGC CATTCTCCTC
37751 TTCAACCTTC ACTACCACTG ATTCTTCAAC CATCCCAGCC CTCCATGAGA
37801 TAACTTCCTC TTCAGCTACC CCATATAGAG TGGACACCAG TCTTGGGACA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

37851 GAGAGCAGCA CTACTGAAGG ACGCTTGGTT ATGGTCAGTA CTTTGGACAC
 37901 TTCAAGCCAA CCAGGCAGGA CATCTTCAAC ACCCATTTTG GATACCAGAA
 37951 TGACAGAGAG CGTTGAGCTG GGAACAGTGA CAAGTGCTTA TCAAGTTCCT
 38001 TCACTCTCAA CACGGTTGAC AAGAGAATGC GCATGGCGAG AAGGGAGAAG
 38051 TGTAGTTGGA TGGATAAAAG GAAGAATGGA GAGAAGAGTG AATGGAAGGA
 38101 AGCAAAGATG AAGCGGAGGA AGGATAGATG CACAGAAGGA AGGATGAAAA
 38151 GAAAGAAAGA TGATGGAAGA CAGGATTGAA GGGGATATAG ATTGAAGGAA
 38201 AGAAAGGTAG AAGGATGAAA TGAAGTAAAG ATTGAAGAAA AGATGGATGG
 38251 AAAGAAGAAA GGAGGGTGCA CAAAAAATCT CACACTTCAC CACATATGAT
 38301 TCATCCATAT AAGAAAAAAC CACTTGTACC CTCAAAGCTA TTGAAATACA
 38351 AACTTTTAAA TTAAAATTTT AAAAAGCAAG AGAAAGGAAA GAAGGGAGGA
 38401 AAGACAAAAG GAAGAATGGG TGATAGAAGG AAAGAATAAA AGGAAGAAAA
 38451 AATGGAAGAA TAGATGATCA GATCTAGGGA TGAATGAAAG GAAGGATGGA
 38501 CAAATCTATA GGTAGGTGGA TGGATCTATG GACAGGTGTG GCCACTTATG
 38551 GCACATAGTC CCAGCTCCAG TTCATACTGA TGGACTTGAG GAGTGTTTGT
 38601 GGCCAATGAA GTGGATCCAT TTAGACAGTG CTCTTCTTCT GAATGAGATG

Exon 5

38651 AGTTACCCCA GTTTTTCTCC CCACCTTCAT CTTCAGGAAC TGATGGCATT
 38701 ATGGAACACA TCACAAAAAT ACCCAATGAA GCAGCACACA GAGGTACCAT
 38751 AAGACCAGTC AAAGGCCCTC AGACATCCAC TTCGCCTGCC AGTCCTAAAG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
38801	GTAGGTTTAA	CTTTGCTTAC	CTCCCAGTAA	TGCCACTCGT	GACCATATTT
38851	CCTCCTCCAG	AGAGACAAAA	TGTTTGTATT	CTTTAGAGAG	AGAATTGTGT
38901	GTGGTTGTCA	TAGGTTTCCC	TGTCTGAACT	GAGTCTTTAT	CTAATGGTTA
38951	CCAGGCAGAT	GTTACCACTG	TCTCTTTCTC	CTCATGGCAT	GCTGAGTGAG
39001	TTTTGTCCAA	CATCAAATAT	TCACAAATTT	GTCCATATTA	ACCAAATTTT
39051	AAAAATGCTC	ATTAAAAACT	TACTATGAGC	TGGGCGCAGT	GGCTCATGCC
39101	TGTAATCCCA	ATACTTTGGG	AGGCTGAGCT	GGGTGGATCA	CCAGAGGTCA
39151	AAAATTGAG	ACCAGTCTGA	CCAAAATGGT	GAAACTCCAT	CTCTACTGAA
39201	AATATAAAAA	TTAGCCGGGC	ATGGTGGCAC	ACACCGTAAT	CACAGCTACT
39251	CAGGAGGCTG	AGGCAAGAGA	GTCACCTGAA	CCACAGGAGG	TAGAGGCTGC
39301	AGTGAGCTGA	GCATTGTGCC	AATGCACTCC	AGCCTGGGTG	GCAGAGCAAG
39351	ACTCCAGCTC	AGAAATAAAT	AATATATTAT	ATATATATAT	ATATGTTTTA
39401	TTTAGATGGA	ATATACTATA	TATATATGTA	TATATATATG	TATGTATATA
39451	TATATATGTA	TGTATATATA	TATATATATA	TATATATATA	TATATAGAGA
39501	GAGAGAGAGA	GAGAGAGAGA	GAGAGAGACA	GAGTATGTCT	GAGAATGCAT
39551	CCCGATAGTT	CTAGCAAGGT	AGGAAAAGGA	AGTATCATAA	CAGCCTTGAA
39601	GTAGCCTGTT	GAAACAGACA	GACTCTCTTG	TAAGAGAACT	CACAAAATCT
39651	AGGATTATAT	CTCCCATGAT	GAAAAATTTG	GAACTGTACA	TTTTTGTTTA
39701	ACTGTCACTT	AAATNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
39751	NNNNNNNNNN	NNNNNNNNNN	NCCAGGAGGC	ACTGTGCTTG	GCGCCTTTTT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

39801 ACCAACACTT TGAGATGGCC ATTGTACTTA TCCCCACTTT ATAGACGGGA
 39851 AAATGGAGGT CCAGCAATAT TTTTAACTT AAAGAGCCAC CCATCTCTTT
 39901 AGAGAAAGAG CCAGAATCCC AGGCAGGGGC TATCTTATTC CAGAGCCCAA
 39951 GCTCTCAAAC ACATGATACA CAATACTTAA TCTCTCTCAA GTCAGAGGAG
 40001 ATCCACTTAA GTATACATCC ATCCACATAT TCATTCATTC AATCATTCAA
 40051 CAAATATTAG TTGAGCACTT ACCGTATGCC AAACAGTCAA ACGTGAATAG
 40101 CTGTTACAAA TGAGACTGTG AAGGATGGTA CAACGCAGAT TCAGACAGTG
 40151 TGATAAGGAA ATATTGAGAA GCAAAGATGA GTTCTGGAGT GAATTTGTAA
 40201 AGGTGGATGT GGGCTTGGAT TTCAATAATG GCAGAACTTA AGGAATCTGA
 40251 TGAGAAGTGG GCACTTCAGG CAGAGAGAAG AGCTTGAACA AGGCTCAGAG
 40301 GCTGACAGTG CAGGAAACAC ATGGGAAGAG GGAATAGAGT AGCGGTCAAG
 40351 AATTCACAGA GGAGTTATAG GTGAAGATGC AACCAAGTTA CAGACCAAGG
 40401 TAAGATAGGG GAATACCAAT CACAATCTCT TTTCCCATTC CAGAAGCATC
 40451 CCAGACACAT CCTAGTAACC GAGAGACATT TCTCTCCCTT TCCTCCTGTG
 40501 GAGAATAAAT AAGCTATTGC AAGTCCAGTA AGTGTAATCA TTTTGTTCAA

Exon 6

40551 ATTGTGTGCC CATTCCCCAA TTTACAGGAC TACACACAGG AGGGACAAAA
 40601 AGAATGGAGA CCACAACCAC AGCTCTGAAG ACCACCACCA CAGCTCTGAA
 40651 GACCACTTCC AGAGCCACCT TGACCACCAG TGTCTATACT CCCACTTTGG
 40701 GAACACTGAC TCCCCTCAAT GCATCAATGC AAATGGCCAG CACAATCCCC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)	
40751	<u>ACAGAAATGA TGATCACAAC CCCATATGTT TTCCCTGATG TTCCAGAAAC</u>
40801	<u>GACATCCTCA TTGGCTACCA GCCTGGGAGC AGAAACCAGC ACAGCTCTTC</u>
40851	<u>CCAGGACAAC CCCATCTGTT TTCAATAGAG AATCAGAGAC CACAGCCTCA</u>
40901	<u>CTGGTCTCTC GTTCTGGGGC AGAGAGAAGT CCGGTTATTC AAACCTCTAGA</u>
40951	<u>TGTTTCTTCT AGTGAGCCAG ATACAACAGC TTCATGGGTT ATCCATCCTG</u>
41001	<u>CAGAGACCAT CCCAACTGTT TCCAAGACAA CCCCCAATTT TTTCCACAGT</u>
41051	<u>GAATTAGACA CTGTATCTTC CACAGCCACC AGTCATGGGG CAGACGTCAG</u>
41101	<u>CTCAGCCATT CCAACAAATA TCTCACCTAG TGAAC TAGAT GCACTGACCC</u>
41151	<u>CACTGGTCAC TATTTCTGGGG ACAGATACTA GTACAACATT CCCAACACTG</u>
41201	<u>ACTAAGTCCC CACATGAAAC AGAGACAAGA ACCACATGGC TCACTCATCC</u>
41251	<u>TGCAGAGACC AGCTCAACTA TTCCAGAAC AATCCCCAAT TTTTCTCATC</u>
41301	<u>ATGAATCAGA TGCCACACCT TCAATAGCCA CCAGTCCTGG GGCAGAAACC</u>
41351	<u>AGTTCAGCTA TTCCAATTAT GACTGTCTCA CCTGGTGCAG AAGATCTGGT</u>
41401	<u>GACCTCACAG GTCAC TAGTT CTGGGACAGA CAGAAATATG ACTATTCCAA</u>
41451	<u>CTTTGACTCT TTCTCCTGGT GAACCAAAGA CGATAGCCTC ATTAGTCACC</u>
41501	<u>CATCCTGAAG CACAGACAAG TTCGGCCATT CCAACTTCAA CTATCTCGCC</u>
41551	<u>TGCTGTATCA CGGTTGGTGA CCTCAATGGT CACCAGTTTG GCGGCAAAGA</u>
41601	<u>CAAGTACAAC TAATCGAGCT CTGACAAACT CCCCTGGTGA ACCAGCTACA</u>
41651	<u>ACAGTTTCAT TGGTCACGCA TCCTGCACAG ACCAGCCCAA CAGTTCCCTG</u>
41701	<u>GACAACTTCC ATTTTTTTTCC ATAGTAAATC AGACACCACA CCTTCAATGA</u>

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

41751 CCACCAGTCA TGGGGCAGAA TCCAGTTCAG CTGTTCCAAC TCCAAGTGT
41801 TCAACTGAGG TACCAGGAGT AGTGACCCCT TTGGTCACCA GTTCTAGGGC
41851 AGTGATCAGT ACAACTATTC CAATTCTGAC TCTTTCTCCT GGTGAACCAG
41901 AGACCACACC TTCAATGGCC ACCAGTCATG GGGAAGAAGC CAGTTCTGCT
41951 ATTCCAAGTC CAACTGTTTC ACCTGGGGTA CCAGGAGTGG TGACCTCTCT
42001 GGTCACTAGT TCTAGGGCAG TGACTAGTAC AACTATTCCA ATTCTGACTT
42051 TTTCTCTTGG TGAACCAGAG ACCACACCTT CAATGGCCAC CAGTCATGGG
42101 ACAGAAGCTG GCTCAGCTGT TCCAAGTGT TTACCTGAGG TACCAGGAAT
42151 GGTGACCTCT CTGGTTGCTA GTTCTAGGGC AGTAACCACT ACAACTCTTC
42201 CAACTCTGAC TCTTTCTCCT GGTGAACCAG AGACCACACC TTCAATGGCC
42251 ACCAGTCATG GGGCAGAAGC CAGCTCAACT GTTCCAAGT TTTACCTGA
42301 GGTACCAGGA GTGGTGACCT CTCTGGTCAC TA TTCTAGT GGAGTAAACA
42351 GTACAAGTAT TCCAAGTCTG ATTCTTTCTC CTGGTGAACT AGAAACCACA
42401 CCTTCAATGG CCACCAGTCA TGGGGCAGAA GCCAGCTCAG CTGTTCCAAC
42451 TCCAAGTGT TCACCTGGGG TATCAGGAGT GGTGACCCCT CTGGTCACTA
42501 GTTCCAGGGC AGTGACCAGT ACAACTATTC CAATTCTAAC TCTTTCTTCT
42551 AGTGAGCCAG AGACCACACC TTCAATGGCC ACCAGTCATG GGGTAGAAGC
42601 CAGCTCAGCT GTTCTAACTG TTTACCTGA GGTACCAGGA ATGGTGACCT
42651 CTCTGGTCAC TAGTTCTAGA GCAGTAACCA GTACAACTAT TCCAAGTCTG
42701 ACTATTTCTT CTGATGAACC AGAGACCACA ACTTCATTGG TCACCCATTC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

42751 TGAGGCAAAG ATGATTTCAG CCATTCCAAC TTTAGCTGTC TCCCCTACTG
42801 TACAAGGGCT GGTGACTTCA CTGGTCACTA GTTCTGGGTC AGAGACCAGT
42851 GCGTTTTTCAA ATCTAACTGT TGCCTCAAGT CAACCAGAGA CCATAGACTC
42901 ATGGGTCGCT CATCCTGGGA CAGAAGCAAG TTCTGTTGTT CCAACTTTGA
42951 CTGTCTCCAC TGGTGAGCCG TTTACAAATA TCTCATTGGT CACCCATCCT
43001 GCAGAGAGTA GCTCAACTCT TCCCAGGACA ACCTCAAGGT TTTCCACAG
43051 TGAATTAGAC ACTATGCCTT CTACAGTCAC CAGTCCTGAG GCAGAATCCA
43101 GCTCAGCCAT TTCAACAACT ATTTACCTG GTATACCAGG TGTGCTGACA
43151 TCACTGGTCA CTAGCTCTGG GAGAGACATC AGTGCAACTT TTCCAACAGT
43201 GCCTGAGTCC CCACATGAAT CAGAGGCAAC AGCCTCATGG GTTACTCATC
43251 CTGCAGTCAC CAGCACAACA GTTCCCAGGA CAACCCCTAA TTATTCTCAT
43301 AGTGAACCAG ACACCACACC ATCAATAGCC ACCAGTCCTG GGGCAGAAGC
43351 CACTTCAGAT TTTCCAACAA TAACTGTCTC ACCTGATGTA CCAGATATGG
43401 TAACCTCACA GGTCCTAGT TCTGGGACAG ACACCAGTAT AACTATTCCA
43451 ACTCTGACTC TTTCTTCTGG TGAGCCAGAG ACCACAACCT CATTTATCAC
43501 CTATTCTGAG ACACACACAA GTTCAGCCAT TCCAACCTC CCTGTCTCCC
43551 CTGGTGCATC AAAGATGCTG ACCTCACTGG TCATCAGTTC TGGGACAGAC
43601 AGCACTACAA CTTTCCCAAC ACTGACGGAG ACCCCATATG AACCAGAGAC
43651 AACAGCCATA CAGCTCATTC ATCCTGCAGA GACCAACACA ATGGTTCCCA
43701 GGACAACTCC CAAGTTTTC CATAGTAAGT CAGACACCAC ACTCCCAGTA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

43751 GCCATCACCA GTCCTGGGCC AGAAGCCAGT TCAGCTGTTT CAACGACAAC
43801 TATCTCACCT GATATGTCAG ATCTGGTGAC CTCACTGGTC CCTAGTTCCTG
43851 GGACAGACAC CAGTACAACC TTCCCAACAT TGAGTGAGAC CCCATATGAA
43901 CCAGAGACTA CAGCCACGTG GCTCACTCAT CCTGCAGAAA CCAGCACAAC
43951 GGTTTCTGGG ACAATTCCCA ACTTTTCCCA TAGGGGATCA GACACTGCAC
44001 CCTCAATGGT CACCAGTCCT GGAGTAGACA CGAGGTCAGG TGTTCCTCACT
44051 ACAACCATCC CACCCAGTAT ACCAGGGGTA GTGACCTCAC AGGTCCTAG
44101 TTCTGCAACA GACACTAGTA CAGCTATTCC AACTTTGACT CCTTCTCCTG
44151 GTGAACCAGA GACCACAGCC TCATCAGCTA CCCATCCTGG GACACAGACT
44201 GGCTTCACTG TTCCAATTCG GACTGTTCCC TCTAGTGAGC CAGATACAAT
44251 GGCTTCCTGG GTCATCATC CTCCACAGAC CAGCACACCT GTTTCAGAA
44301 CAACCTCCAG TTTTTCCTAT AGTAGTCCAG ATGCCACACC TGTAATGGCC
44351 ACCAGTCCTA GGACAGAAGC CAGTTCAGCT GTACTGACAA CAATCTCACC
44401 TGGTGACCA GAGATGGTGA CTTACAGAT CACTAGTTCT GGGGCAGCAA
44451 CCAGTACAAC TGTTCCTCACT TTGACTCATT CTCCTGGTAT GCCAGAGACC
44501 ACAGCCTTAT TGAGCACCCA TCCAGAACA GAGACAAGTA AAACATTTCC
44551 TGCTTCAACT GTGTTTCCTC AAGTATCAGA GACCACAGCC TCACTCACCA
44601 TTAGACCTGG TGCAGAGACT AGCACAGCTC TCCCAACTCA GACAACATCC
44651 TCTCTCTTCA CCCTACTTGT AACTGGAACC AGCAGAGTTG ATCTAAGTCC
44701 AACTGCTTCA CCTGGTGTTT CTGCAAAAAC AGCCCCACTT TCCACCCATC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

44751 CAGGGACAGA AACCAGCACA ATGATTCCAA CTTCAACTCT TTCCCTTGGT
44801 TTACTAGAGA CTACAGGCTT ACTGGCCACC AGCTCTTCAG CAGAGACCAG
44851 CACGAGTACT CTAACCTCTGA CTGTTTCCCC TGCTGTCTCT GGGCTTTCCA
44901 GTGCCTCTAT AACAACTGAT AAGCCCCAAA CTGTGACCTC CTGGAACACA
44951 GAAACCTCAC CATCTGTAAC TTCAGTTGGA CCCCAGAAT TTTCCAGGAC
45001 TGTCACAGGC ACCACTATGA CCTTGATACC ATCAGAGATG CCAACACCAC
45051 CTAAAACCAG TCATGGAGAA GGAGTGAGTC CAACCACTAT CTTGAGAACT
45101 ACAATGGTTG AAGCCACTAA TTTAGCTACC ACAGGTTCCA GTCCCACTGT
45151 GGCCAAGACA ACAACCACCT TCAATACTACT GGCTGGAAGC CTCTTTACTC
45201 CTCTGACCAC ACCTGGGATG TCCACCTTGG CCTCTGAGAG TGTGACCTCA
45251 AGAACAAGTA AGAATAACTT TTTTATTGTG GTAAAATATA AATACTATAA
45301 AAATTGCCAT TCTAAACATT TTAATTGTAC AACTCAGCAG TACTAATACA
45351 TTCACATTGT TGTGCAACCC TCACCACTAT CTGTTTTCAA AACTTTTTTT
45401 ATCACCCCAA ACAGGACTGA AGGAATAATT TCCCATTCCTT CATTCTCCCT
45451 AGTGCAGTGG TGCAATCTCG GCTCACCACA ACCTCTGAAC CTCTGTCTCC
45501 TGGGTTCAAG CAATTCTCCT GCATCAGCCT CCTGAGTAGT TGGGACTACA
45551 GGTGCACGCC ACCGTGCCTG GCTAATTTTT GTATTTTTTAG TACAGACAGG
45601 GTTTTACCAT GTTGGTCAGG CTGGTCTCAA ACTCCTGACC TCAGGTGGTC
45651 CACACGCCTT GGCCTCCCAA AGTGCTGGGA TTACAAGTGT GAGAACTGT
45701 GCCCGGCCAT ATCTGTTAGA TCTTACTAAT CCTGTCAAGA GGATTCAGTG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

45751	TCCTTTTTTT	TTTTTCTTTC	TTTTTTTTTGA	TAGAGTCTCC	CTCTGGCACC
45801	CAGGCTGGAG	TGCAGTGGTA	CGGTCTTGGC	TCACTGCAGC	CTCCACCTCC
45851	CAGACTGAAG	CGATTCTCCT	GCCTCAGCCT	CCCGAATAGC	TGGGACTACA
45901	GGCGCGTGCC	ACCACGCCCA	GCTAATTTTT	GCATTTTTAG	TAGAGATGGG
45951	ATTTCACTAT	GTTGGCCAGG	CTGGTCTCAA	ACTCCTGATC	TCAAGTGATC
46001	CGCCCAAGGG	CCTCCCAAAG	TACTGGGATT	ACAGGTAGGA	GCCACCTCAC
46051	CTGGCCCTAT	TTTCGGAATG	GATTTTTTTT	TAATGTTTAA	AATGTCACCT
46101	AAGATTATTG	TGAAGATCAA	ATAAGATAAA	ATCCTAATAA	CCCAAGTAAA
46151	CCACAGGGCT	CCACTTGGAC	CAGTCTCAGA	AGTTTCAAGA	AAATCAGTCA
46201	GACCATCAAA	TGTAAAATAA	GTCTAAATTT	TCTTTGCACT	ATTCACAGAG
46251	TGCCAAAGAG	GATCTAATTC	ATGTTTCAGA	ACATACCCTA	CTTACTAAAA
46301	TCCCCTTTTC	CTCATTTCTT	CTCATTCCTG	AACTTTATCA	TCTCCTGCGG
46351	ACCCCCTAGC	CTCTCCCCTC	CCCATAGTCA	GTCTCTCTCT	CTCTCTTTCC
46401	CTCCCCTCTT	ATTATCTCAA	TTTCACACGA	AAGAATTCCA	GAAACTATAC
46451	TGCCAAAAGT	CTTTCCTGTC	TTTGAAAAGT	TGGGAAAGAG	GAGAAACTCA
46501	GACAGCAATG	ACAAAATTAT	ACGTAATGGA	TGAAGGAAAC	ACAAATAAGG
46551	CTGGAAACAG	AAAATTTTGT	CCCCATCATT	TATTTAATGA	AGGTGGCAGT
46601	ATTCCAGCCA	CATAGTGAAC	CCCCACAATA	AGAAGGGGCC	TCTGGCGATT
46651	GATTATTGTC	ATTGTTGTTA	ATGATAATGA	GGGTGAGGAT	ATCATGAGCA
46701	TCAGTGTAGG	AGGCAGTTAA	CTAATAAGAC	CAAGCTGTTG	GCTGGGCGTG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

46751 CTGGTTCACA CCTGCAGTCC CAGCACTTTG GGAGGCCAAA GTGGGTGGAT
 46801 CACTTGAGGT CAGGAGTTCA AGACTAGCCT GGCCAACATG GTGAAACCTG
 46851 GTCTCTACCA AAAATACAAA AATTAGTCAG GTGTGGTGGC GTGTGCCTGT
 46901 AATGACAACT ACTTGGGAGG CTGAGGCAGG AGAATCACTT GAACCTGGGA
 46951 GGCGGAGGCT GCAGTGAGAT GAGCTTGAAC CACTGCACTC CAGCCCGGGC
 47001 AACAGAGAGA GACTCTTGTC TCAAAAAACA AAACAAACAA ACAAAAACTA
 47051 AACCAAACAA AAAAAGACTA GCTGTTATTC ATTTATTTAT TTATTTATTT
 47101 AGAGACGGAG TCTCGCTCTG TCACCCAGGC TGGAGTGCAG CGGCACAATC
 47151 TTGGCTCACT GCAACCTCTG CCTCCCAGGT TCATGTGATT CTCCCGCCTC
 47201 AGCCTCCCCA GCTGTTGTTA TTCATGAATG AACCTCAGAG AAAGCACACA
 47251 GGAGGGTTGG TGCACCTGTG TTTTGAGTTC TACCCCTCCT TCCTCTCTTA
 47301 ACTTCCTCCT GTCTTCTCAC TCTGATTCTG TCTTCCTTCC TCTCCCTCTC

Exon 7

47351 TCTCTGCAGG TTATAACCAT CGGTCCTGGA TCTCCACCAC CAGCAGTGAG
 47401 TAAACATGGC CCTGAAGTCC CTATGCCCTG GGAATTCTTC CTCCCTAAGC
 47451 CTGCCTTCCA GGAGGAAAGT ATCCCCCATT CCCTAGGTTC TCATCCCCAC
 47501 AGAAACTCCA GAATAGCAAA AGTCTCAGGC TGAGCCAAGG CACAGATGCC
 47551 AGTGCTCACC AAGAGTCCTA TTCTCCCCTC GCTAAATGAT AGGACCCAAC
 47601 AAACCCGATT CACGCTGCGT TTTCTTTTCTCAG CTCCGATGAC CTCCATGTTC
 47651 TCTCCAAGGC CTCTCGTATC TGTGAGCCCC ACCCCCAGCG CTACAGGTAG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

47701 GAATCTGGCT TCCAGCTCCC ATGAAACGTC GGCTGCCATT CAGTGGCTGA
 47751 TTAATTGCTG TGTGGTCTGA GTCCTGATGC CCACCAAGTC TCAGCGTGTT
 47801 CCCCTCTGTC CAATCTCATC CAACAATTTA AGCTAATGCT TGTTTAATGA
 47851 TGTCTCACT ATACCACCTT GGACACTTTC TTTTGCCTG GATTTAAAGC
 47901 TTCCATTTCT TTCCTTCCTT CCTTCTTTTC TTCCTTCCTT CCTTCCTTCC
 47951 TTCCTTCCTT CCTTCCTTCC TTCCTTCCTT CCTTCCTTCC TCCTTCCTTC
 48001 CTTCTTTTCT TCCTTTCTTC CTGTCTTTTT CTTTCTTTCC TTCTTTTGGC
 48051 AGAGTCTCAC TCTGTCGCCC AGGCTGGAGT GCAATGGTGC AATCTCGGTT
 48101 CACTGCAACC TCTGCCTCCC AGGTTCAAGC GATTCTCATG CCACATGCCA
 48151 CTATGCCTGG CTAATTTTTG TTTTTTTGTT TTTTGGGGG TTTTTTGAGA
 48201 CAGAGTCTCA GTCTGTTGCC CAAGCTGGAG TGCAGTGGCA TGATCTCGGG
 48251 TCACTGCAAC CTCCTTCTCC CAGGTTCAAG CGATTTTCCT GCCTCAGCCT
 48301 CCTGAGTAGC TGGAAC TACA GGCACGCACC ATCACACCGG CTAATTTTTT
 48351 GTGTTTTTAG TAGAGACGAC GGTTTTGCAA TGTGGGCCAG GCTTGTCTCG
 48401 AACTCCTGAC CTCAAGTGAT CCTCCAGCCT CGGCCTCTCA AAGTGCTGGG
 48451 ATTACAAGTG TGAGCCACTG CACCAGGCCA AAAACTTGTA TTTCAATAGT
 48501 CATTGAGGCT GGGTGCAGTG GCTCACGCCT GTAATCCCAG CACTTTGGGA
 48551 GGCTGAGGCC AGTGGATCAT GAGGTCAGGA GATCAAGACC ACCCTGGCTA
 48601 ACACAGTGAA ACCCCATCTC TACTAAAAAT ACACACAAAA ATTAGCCGGG
 48651 CATGGTGGCA AGATGCCTGT AGTCCCAGCT ACTCAGGAGG CTGAGGCAGG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
48701	AGAATGGCGT	GAACCTGGGA	GGCAGAGCTT	GCAGTGAGCG	GAGATCGCAC
48751	CGCTGCACTC	CAGCCTGGGC	AACAGAGAGC	GACTCTGTCT	CAAAAAAAAA
48801	AATATATATA	TATATATATA	TATATTCATT	GAGACCGACT	CTGACTTAAA
48851	AGCAGTAATG	AATGGTGTAG	GTTTGGTAA	ATTACAGGTC	TTGCTTTAAG
48901	TCCTGGTCCT	CTCTTTTGCT	CACTGTGTGG	CCCCGGAAGA	GCCATGTAAC
48951	CTCTCCAGGC	TTCAGTGTCC	ATTTT'TAGAA	CGGAGTAAGT	GAATAAGCTG
49001	TGTCCAATCA	TCTCTGGCCA	TATCAGCTTC	ATTTTTTTTT	TCCTCCAGGG
49051	TCCAAACATC	CCTCCACCCT	CAGAGTCTTT	GCACCTGGTG	TTCTTGTCTT
49101	TCAAATCTCA	GCTTGGATCA	CCCTTTATAA	AGTAGCATTT	CCCCCGTATA
49151	CGCATCTTGC	ACACAGCCAA	TCTCTATTCT	ACCTCTATGC	TCACTTCCTT
49201	CCTGGCAATT	ATTACTACAG	CTGGGCCCTT	GAACAGCATG	AGGGTTCAGG
49251	GTGCTGACCC	CTATGCATTC	AAAAATCCAC	ATATAACTTT	TTTTTTTTTG
49301	AGATGGAGTT	TCACACTTGT	TGCCCAGGCT	GGAGTGCACT	GGCGCCATCT
49351	TGGCTCACTG	CAAACCTCTG	CTCCTGGGTT	CAAGTGATTG	TCCTGCCTCA
49401	GCCTCCTGAG	TAGCTGGGAT	TACAGGCATG	TGCCACCATG	CCCAGCTAAT
49451	TTTGTATTTT	TAGTAGAGAT	GAGGTTTCTC	CATGTTGCGC	AGGCTGCTCT
49501	TGAACTCCTG	ACTTCAGGTG	ATCCGCCTGC	CTTGGCCTCC	CAAAGTGCTG
49551	GGATTACAGG	CATGAGCCAT	GATGCCCCGC	CATTGCTAA	TGGCATCTAG
49601	TAAGTAGAGG	CCAGAGATGT	TGCAAAACAT	CCAACAATGC	ACAAAGCAGC
49651	CTCCTATCAA	AACACATTAT	CCAGACCAAA	ATGTCAATAG	GGCTGAGGTT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

49701 GAGCATCTGC TGTACACAGA TTCCAAGTTC TGGTACAAAT CTCGTAGTTC
 49751 TCTGAGGGCT CATCTTTCAA TGCCTAGCAC ATCAAAGGAG GCCAATTTCC
 49801 TCTTCCCTTT CACCTCCTGG TATGAAATGT TTCCTCCTCC ACCTTGATCC
 49851 TGTAAGAGCC CAGCTGGAGT TTGCAGACGA CGGGGAAAGA AATGGGTGAG
 49901 GGAGGGTCCT ATGGTTGAGT CTCCGCAGTG GGCCCTGGGT GCCCAGTTCA
 49951 CCCTCCTCCC CTTCAATTTT TCCATCATGA CAACTCAAGG CAAATTCTCA
 50001 GTTTCCATGG GCCAGTGGAA TCCACTGACT TCATGAAATA ACCCCACCCT
 50051 GAGCAAATAC CCCTCAAATA ATAAGTGTTC ACACAACATC AGTGGCAACA
 50101 ATGACCCAAG CAGCAATGCC ACCACCAGAA TAGCAACCAT AACAGCAGCT
 50151 CATTTTCATC AAAAGGAAAC TGTAGGGCCA GGCACAGTGG CTCACACCTA
 50201 TATTCCCAGC ATTTTGGGAG GCTGAGGCAG GCAGATCACC TGAGGTCAGG
 50251 AGTTCAAGAC CAGCCCAGCC AACATGGTGA AA CCAATCT CTACTAAAAA
 50301 TACAAAAACT AGCCAGGCTT GGTGGCATGT GCCTGTAATC CTAGCTACTC
 50351 GGGAGGCTGA GGCAGGAGAA TTGCTTGAAC CTGGGAGGCA GAGGTTGCAG
 50401 TGAGCTGAGA TTGTGCCACT GCACTCCAGC CTGGGCGACA GAGCAAGACT
 50451 CCGTCTGAAA AAAAAAAAAA AAGGAATTGT GCCAGGAATT GTGATGAGAA
 50501 CTTTATATGC ATTATCTCCT ATTAATATTA CCCAAACCTC CGTGAGTTAC
 50551 TATACTCATT TCTACAGAGA GCATTTATGC ATCCAGGGAG GAAGTAATTA
 50601 GCCCAGAATT ACTCAGTTAT GACACAGGAC AGTATGAAAA CTCCAACCGA
 50651 AGATTGGAGA CTCATGAAAA CTCCAGGCTC CTAAGTACAA GACATCACTG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

50701 TGGATCGTCC AAATAGAGCA AGCCCCAATC TCAGGACAGG AATGAGGCAT
50751 GAATGGCCTC TATGCTAATG ATCTAACCTA ATGCTGAATT TGTTACTTCC
50801 CTTCTGAATC CACTTGGAGA TTTCTTTTAT ATCTGACTTG AAATAGAGGA
50851 TATATACTCC TCTATCCTTG ACATAGGAGA TAATACACAG AAAGTATTTT
50901 ATTGTAGTAT CAAGTACACA TCCTGTTCTG TGTCCATAGG ATTATGACTA
50951 ATTTAGGGCA TGGCTTAACA GTGTGGTACT ATTGAATGAC AGACAGATGT
51001 CTGTTTTGTT GGATGCAGGA CAAGCCATGT AACCTCCCCA GACTTTAGTG
51051 TCCCCTCTGT GGAATGGAAT AAAAATACTA CGTGGGATTG TTCTGATAAT
51101 CAAATGAGAT AATTCAGGAA CAACCCAGAT AAATAACAGG GCTGCCCTGG
51151 GTTCTGTCTT TCCTTGTATC TCTCACAGAG CCTCAAAGGA GATGCAATCC
51201 ATGACCTAGA GAAACACTCA GGACAAATTC TCTTTTCCCC AGTTCCTTTC
51251 TTGCTCCAAT GGCAACACCA CCCCTCTCAT CCTGAAGTCT CTTGTTTTTA
51301 CCACCACACC TATTTTGCCA AATTTTCTCC AATATTCCAA ACCATATGAA
51351 ACCTTTCTTT CTTTCTTTTC TTTCTTCCT TTCCTTCTTT CTTTCTTTTT
51401 TCTCTTCTTT TCTTTTCTTT TTGAGACATG GTCTCACTCT GTTGCACAGG
51451 CTGGAGTGCA ATGGCACGAT CTTTGCTCAC TGCAACCTCC GCCTCCCAGG
51501 TTCAAGAGAT TCTCTGCCT CAGCCTCCTG AGTAGCTGGG ATTACAGGCG
51551 CCCACCGCCA CGCCACGCTA ATTTTGTGT TCTTAGTGGA GACGGGGTTT
51601 CGCCATGTTG GCCAGGCTGG TCTTGAATC CTGACCTCAA GTGATTTGCC
51651 CATCTCGGTC TCCCAAAGTG CTAGGATTAC AGGCGTGAGC CACCAAGCCC

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

51701 GGCCCCATAT GAACCGTTTC TATCCCTCAT TTCTCTGTAC TTTTACCTAA
51751 AAACACCACT CCCTTCACCC ATCACATTTT TGTCAATTCT ACATCACACA
51801 CACACACACA CACACACACA CACACACAGA GAAAGTAAGT TGGAAAAAAA
51851 TTATACTATC ATGAAATTTT GTGAAAGGAG GTAAGCTGAG AGAGTAAGAA
51901 TCAAACATAA TTATCTTTAT GGGTAGAAAG CACACTCATC CATACATGTG
51951 TCTTTCACCC CTTGTAATGT ATTTATTATT ATTGTTTGTA TATACTAGAT
52001 TCCCAATAAA TAGGGACAGC TATTATGGTA TTTTATTTC AGGAATAATA
52051 ATAGTGATGA TTTCCACCAT TATTGTCAA GGACAAAGCA CAAAATATGT
52101 ACCAAATAAA ATATAGCCAT TATCCTTTAT TCACAAAAGA TCTTGGCCCC
52151 ACCTCTTCTC AATGAAATGT CCATGACTTG TTCAACTTTG GCCACTCTGG
52201 GCTGAGAGAT GGAGGTTCCT TTGCGAGCTG AAGTCACACA TCGAAGGTGG
52251 AAGCCCCTCC CCTCCCTCTG GCTGGCTGAG GGATAGCCCA GATGGGCTCA
52301 TCATGAAAGT TTCCCATTAT TTCCATTTCT GGATCTACCA TCTTCCCCTC
52351 CCCTACCTCT CACCCATCAT AATTGTCCTT CTTTACTCTT TCCTCCCTAT

Exon 8

52401 CTGCAGGTTA TAACCGTCGG TACTGGACCC CTGCCACCAG CAGTGAGTAT
52451 TCAAACCTGT GATATTCCAA TGCCCTTGGG ACCCTTCCTC CCCAAGGTGC
52501 ATTCCTCAGA AGAGAACTG ATCATTCTCC CTCCCTACGT GCCCAGCCAC
52551 AGCCTCAGAG CAGCCCCTAA CCCGTCAAGG TCTTGGTGTG AGTCAAGATA
52601 GAAGTCCAAA TTCCAATGAG CAGTTCCTGT CCCATATTCC TTTAGGAAGA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

Exon 9

52651 CACCCAATCA TTTCTCCATG TTCTTTTTTT CTCAGCTCCA GTGACTTCTA
52701 CATTCTCCCC AGGGATTTC ACATCCTCCA TCCCAGCTC CACAGGTAGG
52751 AAGCTCCTCT CTGGCATCTA TGAAATTTAA CACTGCATGG TCTGTTCCCT
52801 GCTGACCACC CAGACTCAGC CTGTTCCACT CGCCCTCTCA CTCTCTCTCT
52851 CTCTCTTTTT TTTTTTTTTT TTTTTTTTTT TTTACGGAGT CTTGCTCTGT
52901 CACCCAGGCT GGAGTGGAAT GGTGTGATCT CGGCTCACTG CAACCTTCGC
52951 CTCCCAGGTT CACGTGATTC TCCTGCCTCA GCCTCCGGAG TAGCTGGGAT
53001 TACAGGTGCA CACCACCATG CCTGGCTAAT TTTTGTATT TTTAGTAGAG
53051 ACGGGGTTTC ACCATGTTGG CCAGGCTGGT CTTGAACTCC TGACCTCAAG
53101 TGATCTACCC ACCTTGGCCT CCCAAAGTGC TGGGATTATA GGCATGAGCC
53151 ACCACGCCAG GCCCACTCTC TAAATTTTGA CCACCCTGCC TTGAGTGGTC
53201 TTCTAGCACC CTAACCTCTG TCTAACCTCG AGAGCTTTGC ACTAGCGATT
53251 CCTGGGGACC AGCTATGGTT GGTATCTTCT CAACTTTCTA ATTTTTTTAA
53301 AATTATTATT ATTATTATTA TTATTTTAAA TGGAGTCTCG CTCTGTCACC
53351 CAGGCTGGAG TGCAGTGGCA CCATCTCGGC TCATTGCAAC CTCTACCTCC
53401 CGGGTTCATG CAATTTTCCT GCCTCAGCCA GAAATTTTCT CAGTGGTCGA
53451 GATTGTGCCA CTGCACTCCA GCCTGGGCAA TGGAGCTAGG CTCCATCTCA
53501 AAAAAAAAAA AAAAAAGACG GAGGTCGGGC ATTCTAACC CTTAACCTG
53551 CCTTGTGATT CTGGAGTTAT GAGATAGAAC CTGGTGTCCC GTAATTAAAA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
<hr/>					
53601	TTCCGCCTTC	AGGCCTTATG	TTTTGTGAGT	CACAACACTG	CAAACCTTTT
53651	ACATGCTGTA	GACAGGATGT	TCACTCTCCA	CTTCCTCACT	GCTCTGCTCT
53701	AATCAATTCA	ACCATTTATG	TGACATGCCT	AACCCCTCTG	GGCTTGTACG
53751	TATGTAACAT	GTATTACAAA	GCAAGTCATT	CCATGATCAA	TGCTGTCACT
53801	TTTTCTAGGT	GCTTTCAAAA	TTTGTTCTTC	ATCATTGATT	TTCAGTAGTT
53851	TGATTACGAT	GTGTCTGGGC	ATGGTTTTCT	TTGAGTTTAT	CCTGCTTAAA
53901	GTGTTCTCAG	CTTCTTGAGT	CTCAAAGTGT	TTATTTTCTG	CTCTGATTCT
53951	TTCTCCCCTT	CGGACCTCCA	ATGAAATGAT	GTTGCCCGAA	GAGACCCTGA
54001	GGTTCTGTTC	ATTTTGTTAT	TTATCAATCT	TTTTTCCTCT	CCGAATTTCA
54051	GGTTTAATAA	TTTTTTTTTT	TTTTTTGAGA	CGGAGTCTCG	CTCTGTCGCC
54101	CAGGCTGGAG	TGCAGTGGCG	CGATCTCGGC	TCACCGCAAG	CTCCGCCCCC
54151	TGGGTTACAG	CCATTCTCCT	GCCTCAGCCT	CCGGAGTAGC	TGGGATTACA
54201	GGCACCCGCC	ACCATGCCCC	GCTAATTTTT	TGTATTTTTT	AGTAGAGACG
54251	GGGTTTCACC	GTATTAGCCA	GGATGGTCTC	AATCTCCTGA	CCTCGTGATC
54301	CGCCCGCCTC	AGCCTCCTAA	AGAGCTGGGA	TTACAGGCGT	GAGCCACTGC
54351	GCCCGGCCCA	GGTTTAATAA	TTTTTATAGA	ATATTTTCAC	AATCACCAAG
54401	CCTTTTCTCT	ACCAGCTCCA	TTCTGCCCAT	CCATTGAATT	CTTTTTATCT
54451	CAGTTACTTT	ATGTTTCAGT	TCGAAAGTTT	CTACTTGGTT	AGATAGATAG
54501	ATGTTATATC	ATATATTATA	TGTTATATAA	AAATATATTT	ATGGTTATAC
54551	ATATAACATA	TATGTTATAT	ATAGTTATTT	ATATAGCCAT	AACTATATAT

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence
(SEQ ID NO: 1)

54601 AGCCATATAT ATAGTTATAT ATAACCATAT ATATAGTTAC CATATAGTAA
54651 CCACATATAT AAAACATATA TATATAGTGT CTCTCTATAT ATAGTTATAT
54701 ATATAGTTTC TATATCTGTA ACTATATATA GTTATATATG TATGTTTCTC
54751 TGTATATAAA TATATATATT TCTATATATA TAGTTATACA CATTATATAT
54801 ATAAC TGGGA GATGTTGGTA AAGGATGGCG TGAGGAAACC TGGAGCAGTC
54851 ATGGTAATCC TCGCTCTGCT CCGAACTCCT CAAGAGCAGG AGAAGGGTCC
54901 TCCTCATTCT CCAGCCATGT TGA CTTTGAG CAATTTACTC ATCCTCTCAG
54951 TACCTCAGTT TCCTCACCTG CCAATTGAGG ATAATAATAT TTCATAAATT
55001 GTTTGCAAAT GTTATATGCA ACTCTACGTA AGAACACCTA GCACAGGGGC
55051 TACCAGGGAA TTTGGTTTAA CAAATATTTA TCAGGCACCT ATTCTGGGCT
55101 GGGCAGGGGG GATAAGATGT TGA CTTAAGTC AAATGCAGTC CCTCCCCTCA
55151 CCAAGTTTAC AGTGTATTGG GCAAGACTGA AATGGAACAA GCAATTACAA
55201 TTGACAATAA AAGACAACCA AGTTATTGAG CACTTACTAT ATGGCATGCC
55251 ATATGCTATG TATTTTTTTT ATTTTAACT TTTCATTTTG AAATAAATAA
55301 TAAATATAAA GTAAATAATA ATATAAATAA ATAATAAATA ACTTTTCATT
55351 TTGAAATAAA TAATAAATAA ATTCAGGAGA TGTTGCGAAA ATAGTG TAGC
55401 ATTCCCCTGT ATCCTTCACC CAGTTTCTCC CCAATGGCTA CATCTTACAT
55451 AACTCTAATA CAATATCAAA AGCAGGAAAC TGACATTGTT AAAATCCATT
55501 TTA CTTGGTTT TACACGCGTG TGTGCATATG TGAGCTTG TG TATGTGCGTG
55551 TGTGTGCAGG CATGTGTGTG CATGCACGCC TGTGTGTGCA TATGTGCATG

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence (SEQ ID NO: 1)					
55601	TGTGCATGCG	TGTGTGCATG	TGTGCATGTG	TGTGTGCATG	CGTGCGTGCG
55651	TGCGTGCATC	TGTGTGCATG	TATGCACATG	TGTGTGTGTC	TGTGCACGTG
55701	TGTGCATGCA	TGTGTGTGTG	CGTGTGTGTT	GGTAGCCCTA	TGCAATTTTT
55751	ATCACATGGG	CATAGCCCTA	TAATCACCAC	CACCATCAAG	ATTCAGAACT
55801	GTTCCATTCC	CCCAAAGATT	CCCCTCATGC	TAGCCTTCGT	AATCATGCCC
55851	ACTGAGCCCA	ACACTATTGC	ATAGAATAGC	TATTCTACTC	TCCATCTCCA
55901	TCTCTGTCTC	TACAATTTTC	TTTTGAAGAT	GTTATATAAA	TGGAAATGTA
55951	CAACATGTCA	CCTTTGAAAT	TGGCTTCTTT	TCCACTCAGT	GTAATGCCCT
56001	GGAGATGTGC	TCTTTTAAAC	AGTCATGTAA	CCTTCCTAAT	TTCCCTCCAA
56051	AATATCATTA	TGCCCCTCGC	CGCCTTTTTT	TTTTTTTTTT	TTTTTTGAGA
56101	CAGAGTCTCG	CTCTGTTGCC	CAGGCTGGAG	TGCAGTGGTA	TAATCTCAGC
56151	TCACTGCAGC	CTCCGTCTCC	CGGGTTCAAG	GGATTCCCCT	GCCTCAGCCT
56201	CCCAAGTAGC	CAGGATTACA	AGTGCATGCC	ACCACGCCTG	GCTAATTTTT
56251	GTATTTTTAG	TCGAGACGGG	GTTTCATTGT	GTTGGCCAGG	CTGGTCTCGA
56301	ATTCCTGACC	TCAAGTGATC	TGCCCCCTT	GGCCTCCCAA	AGTGCTGGGA
56351	TTACAGGTGT	GAGCCACCGC	GCCCGACCCA	TATTGCCCAT	TGTATTACAG
56401	CGGAAGAAAC	TGAGGTATGG	ACAGGTAACA	TGTCCATGGT	CACTTGGCTG
56451	GTGAGGGGCA	GAGAGGAGAT	TTGAAACCAA	ATCTGACTCA	CTAGTGTGGC
56501	CGTAACCATG	GTAACATATG	CTCTCTACCA	TGTGGTCTCC	TCTTTATTAA
56551	AGGAAGGGCA	AGTTCTGGGA	GTTTTGGGAG	TTTTGGGCTT	GAGTGGGGAA

Table 1 (continued)

Genomic CA125 Amino Terminal Sequence	
(SEQ ID NO: 1)	

56601	GGGTAGCCAA GTAAAGCAGG TGAGAGAAGG TCTGCTTTAA GGACTGCTGT
56651	TTGATTTTAA TTGTTGTTGT TCAGTGTTC AATGGGATTGA GTTGACTCTT
56701	TTTTCCCTTC TTGTTCCCA AAGCATGAGA CTGTTCCGGT CCTTTTCCCT
56751	TTTAACTTCT CAGCTAGAGT TTGTTAGGGC GGGTATGGGC ACCTGGCAGA
56801	GTCTGAGACC TCAGCTTCCA GTAGGCACAC GTTCTGACCC AATACACCTA
56851	CCCTGGTCCC CTAACCTGCT TCTGGTCCCC TAACCTGCTT CTGGGCCCAG
56901	GTAATGCATT TTAGGAACAT CCCACTTTTC TCCTTACCTG GCTTTCCATT
56951	ATCCGTCCAA ACTAAAGCAC CCACCTGTCT GCTTCAGACT CTTGCTTCAA
57001	GCACTCCGTC TGGGTCCTCA GAAATTGACT TACAGTCAGT TCAGATCTGA
57051	CTCAGGCGTG GCCTTCTTTT CTCCTTCCTT GC

Table 2

**Genomic Repeats
(SEQ ID NO: 2)**

ExonR1

1 AGCAGCCACA GTCCCATTC TGGTGCCATT CACCCTCAAC TTCACCATCA
51 CCAACCTGCA GTACGAGGAG GACATGCGGC ACCCTGGTTC CAGGAAGTTC
101 AACGCCACAG AGAGAGAACT GCAGGGTCTG GTGAGAGCCC CGCCCACCGT
151 ACTCCTCCCT CGCCCACTTA GACAAACCAG CCCACCTCAC ACTGCCTCGC
201 CCACTGATGC CAGCCACGCC CACCTCATCC AACCCAGAC ACCTTTCCT
251 GCCCCACCCA CTGATTTTAG CCAAGCCCAC CTCACCCAC CCAGCCTACT
301 GATGCCAGCC ACGCCACCT TTCCCTGCCC CGCCCACTGA TTTCAGCCAC
351 GCCCACCTCA CCCTGGTCCA CCCCTCCAAT GCCCACTCT TCCTGGCTTC

Exon R2

401 CCGCAGCTGT TGTTTCTCAC CTCCCCTCTC CTTCTTGCA GCTCAAACCC
451 TTGTTTCTAGGA ATAGCAGTCT GGAATACCTC TATTCAGGCT GCAGACTAGC
501 CTCACTCAGG TGAGACGCTC CTTAAGAAAA ACACAGCCCA ACAGGTGAAT
551 ATGACCCTAG TCTCTGGGCT CCCTGACTCT GTTCATACTT GGAACAACCTA
601 TTGCCCCTAGG ATACTAAGCA TCACCACCAG CAGCAGCAGA TAACCTATTC
651 TAAGACCCAA GGCCTGCAT TATGTACTTT ATATTTAATG CCTCATCAGT
701 GCTTGCAACA GCCTCATGAA GCAGGAGCAG AAGGGGAAAC TGAGGCCAG
751 ATTAAGTGGC TTGTGCCAGG ACACACAAAG CAACTGCAGC ACTTCAGGTT
801 CTATATCCAA ACTCCTATCC CTTAGGTGGC ACTTCCTCCT CTGCCCCCAT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
851	TATGAACTTG	CAGCATGTGG	AAAACCCCAA	TCTGACTTCC	CTCTAAGGGA
901	ACTTGCCCAG	AGAATCTAAG	AGGGGAGGAA	AGGAAGGCGT	TCAGCCCTTA
951	CAGGCAGGAG	GTCAGCTCCT	GAGTGGCTCA	GATGCAGCCA	CAGAGGGCCT
1001	GGCCGGTCTG	AGGGTGACTG	AGAGGCACCG	AGGGCACTGT	CCCTGAGTGC
1051	TGGAAAGGGC	AGGTCTTTTA	GGGTAGACAG	CGGTTGATAT	CATTTCTCTG
1101	CTGGCATTCT	CACCTTCCAC	ACCTCTCTCA	CAGAATCTCC	AAGTGTGGCT
1151	CTCCAAGAG	AGAGTGTGAG	TCATCTACCT	CCAGCTTCCT	TTCTTCCCA
1201	GGGGGAAGAG	GGGACAGGGG	GGCCCTAGTG	GCTAAGAGCA	TTGGTGAACT
1251	CAGGCAGACC	TCAGTTCTGA	ACCAACCCAG	CTCTGCCATT	TACTATCTGT
1301	GACTCTGAGC	AAGTGCCTGA	AGCCTTCTGT	GCCCTATTTC	CTGACATATT
1351	ATATATATAA	AATACATATA	TTATATATAG	ACATATTTTA	TATACATATT
1401	GAGGCATATT	TTATAACAT	GTTTATAGAC	ACATTTTAT	ATGCATATGT
1451	TATATACGTA	TATAACATAT	GTTATATATA	ATGTATATAT	TATACATATT
1501	GTTATATTGT	ATACATGTTA	TATATGTTAT	AGCATATATA	GTACAAGTTA
1551	TATATAACAC	ATACATTATG	TTACATATAA	TGTATATGTT	ATATATGATA
1601	TATTATATAT	AATTATATAT	TATATAAAAC	TGTTATATAT	AATTATATAT
1651	AATATATAGT	TGTTATATAT	AATTATATAA	TTGTTATATA	TTATATACAA
1701	CATATAACAT	ACATTATATA	TTGTTATATA	TAATATAATA	TATACATATA
1751	TAACATATGT	ATAACTTTTA	TGTTATACAT	AATGTATATA	ACATATATGT
1801	GATGTGTGA	TGTACATAAC	ATATCTGACA	TTAACATATA	ACATATGATA
1851	TAACAATATT	ATATGTTATA	ACATAATATA	TGTTATAATA	TAACAATATT
1901	ATATGTTATA	ACTTATACTG	TCATATGTAA	CATATACATA	ATATTTTATA

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
1951	AATCAGTTTA	ATATACATTA	TGTTACATAT	AATGTATGTT	ATATATGATA
2001	TATTATATAT	AATTATATTA	TACATAATTG	TTATATATAA	TGCATACATT
2051	GTATTTGTTA	CGTATTATAT	GCAACATATG	GGGATCCTCT	AGAGTCGGAC
2101	CAGCGGCAGC	AGCTGCCTGC	CTTTTNNNNN	NNNNNNNNNN	NNNNNNNNNN
2151	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
2201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
2251	ATATACATAC	ATAACATATG	TATAACTTAT	ATGTTATATA	TAAGTATATA
2301	ACATATATGT	GTATGTGATG	TATATAACAT	ATCTGACATT	AACATATAAC
2351	ATATGTTATA	ATATGACATA	TTATATATAT	TACATATAAC	GTATATCATG
2401	TATAATATAA	TGTGTATATA	TAATATATTA	AAGTATATAA	GTATAAATAC
2451	ATGTAATATT	TAAATATATA	TTATATATAG	TATACATGTG	GATACATACA
2501	ACTTCTACAT	ATACCTAGTA	TATATTCTAT	ATATAAACAG	TCCATGAATT
2551	ACAATGATTC	AAC TTATGAT	TTTTCAAAC	TTGTGATAAT	GCCATAGCAA
2601	TATGCATTCA	G TAGAAAGCA	TACCTTCAAC	ACCCATGCAA	CCATTCTGTC
2651	ATTCACTTTC	AGTACAATAT	TCAATAAATT	ATATGAGATA	TTCAACAGTT
2701	TATTATAAAA	TAGGCTTTGT	GTTAGGTGAT	TTTGCCCACA	TGTAGGCTAA
2751	TGTAAGGGTT	CAGAGCATGT	TTAAGGTAGG	ATAGGCTAAC	CTATCATGTT
2801	CTGTAGGTTA	GGTATAGTCG	ATTTT TATTT	TTATTTT TAT	TTTTGAGACA
2851	GAGTCTTGCT	CTGTCACCCA	GACTGGAATG	CACTGGTGCG	ATCATAGCTC
2901	ACTGCAGCCT	TGAACTCCTG	GGCTCAAGTG	ATCCTCCTAC	CTCAGCCTCC
2951	TGAGTAGCTG	GGACTACAGG	TGTGTGCCAC	CACACCTGGC	TATTTTTTTT
3001	TTAATTTTTT	TTTTTTTGTG	GAGAGGAGGG	TCTTGCCATG	TTGCCCAGGT
3051	GGCCTTGAAC	TCCTGGGCTC	AAGGAATCCT	CCCACCTTGG	CCTCCCAAAA
3101	TCCTGGGATT	ACAGGTGTGA	GCCATCACGC	CCGGCTACAG	GGCATT TTTT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
3151	ACTTATGACA	TTTTCAGTTC	ACAATGGATT	TGTCAGGGCT	GGGCATGATG
3201	GCTCACACCT	GTCATCCCAG	CACTTTGGGA	GGCTGAGGCA	GGTGGATCAC
3251	TTGAGGCCAG	GAGTTTGAGA	CCAGGCTGTC	CAAATGGCAA	AATCTTGTCT
3301	CTACTAAAAA	TACAAAAATT	AGCCAGGCGT	GGTGTGACAA	CTGTAGTTCC
3351	AGCTACTCGG	GAGACTGAAG	CGTGAGAATC	ACTTGAACCT	AGGAGATGGA
3401	AGTTACAGTG	AGTCAAGATC	ACACCACCGC	ACTCCAGCCT	GGATGACAGA
3451	GCAAGACTCT	TGTCTCCAAA	AAACAAAAAA	CAGGCTGGGT	GCATGGCTCA
3501	TGCCTGTAAT	CCCAGCAGTT	TGGGAAGCTG	AGGCAGGTTT	ATCACCTGAG
3551	GTCAGTAGTT	CACGATCAGC	TTGGCAAACA	TGGAGAAAAC	CCATCTCTAC
3601	TAAAAATACA	AAAATTAGCT	GGATGTGGTG	GTGGGTACCT	GTAGTCCCAG
3651	CTACTCGGGA	GGCTGAGGCA	GGAGAATGGA	TTGAACCTGG	GAGGCAGAGG
3701	TTGCAGTGAG	CCAAGATCAC	ACCATTGAAC	TCCAGCCTGG	GCAACAGAGT
3751	GAGACTCCAT	CTCCAAAAAC	AAAAGAAAGC	AAAAACAAAA	AAATAAAATA
3801	AAAAACCTGT	GTTTATCAGG	ACATAATACC	ATCATGAGTC	AAGAAGCATC
3851	TAAATGTACA	TGGTAGTTAT	ATAAAAATAG	TTATATAGTT	ATATACAATA
3901	GTTATATATA	AACCAGTTTA	ATATATGTTA	AGTAGAGGTA	TATGGTAGTT
3951	ATATAAAAAA	TAGTTATATA	ATAGTTATAG	AGTTATATAA	TTATATAAAA
4001	TAGTTATATA	TAAACCAGTT	TAATATATGT	TAGGTAGAGG	TATAATAATA
4051	TATATTGTAT	ATACTATATA	ATATAGTAAT	GTATAAAATG	CAAAACGATA
4101	TCATATATTT	CTATATTAAG	TTTATATTTA	CAGATCTACA	TTTTATATAT
4151	TTTATGTTAT	ATACAATTGT	GTTATACATA	ATATAATTAG	TATAGTACTG
4201	ACTTGGGGAA	TTGAGCAGTA	CCAACCCATA	GGGATGTTTG	AGGATGAAAA
4251	TATGTGATTA	TGAATACAAA	ATGCTGGGCC	TGCTGCATAG	GAAGTATTTA
4301	ATAAATGGTA	GTTGTTACTA	TAAAGTCGTT	CCTACTATAG	AGCTACTCAC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
4351	AACCTGGGAC	ATAGGGAAAG	AGCCCGTTTC	CCTCTAATCA	CTCAATAGTG
4401	GGTGGCTAGG	TAGGTGAGTC	CACATCCTGT	GGCCGGGAAC	AGGTGCTGAG
4451	ACATGAAGAC	CTTCTGACTG	CATGTTGGAC	CAGCCACAGT	TTCAGACGGA
4501	CCAGCCAAAA	AGGGCATTTC	CCCCAAGCCA	TTTAGCTCCC	TTGAGTCTCA
4551	TAACAAATCT	CCTAGACCCT	GCTGGTCCAT	AGGATCTAGA	GAGGATGACT
4601	TGAACCTTCT	GATCCCACCA	TTTGAAAACG	CCATGCCATG	GGCACCAGTA
4651	GGAGGGCCAC	TGCTACGTGC	ACCAGTACAA	GGGCCACTGC	CATGGATTAC
4701	AGATTAACCC	TAAGTATAGC	TGTCGCACAC	CTAGTACTTC	AGGAGGCTTA
4751	TTCGGGGCCA	TGCAGATCCC	TGGCATTATT	ATCCTAGGAT	CCTACACCAA
4801	GCAAAGCAGG	AGCTGCCCCCT	CCTCATAAAC	CCATAAGCCC	TCCTCTTGAG
4851	CAAAGCAGCT	GGGAAGGCCA	GAAGTTATTC	AAGCTCCCCCT	CTGCCCCGGT
4901	TCCAAAGACA	GACAGCTCAA	GCCTACATGC	AGCAAACCCT	ATAAAAGTGT
4951	CACCTCTTGG	CATTTCTGCC	ATGGTAATGC	TTTCTGCTTC	CACTAATAAT
5001	CCTAGTAATT	TGTTTATGGT	GGGCATCTCT	CTGATGAGAA	CCACATTCTT
5051	TTTTTTTTTT	TTTTTTTTTT	TTGAGATAGA	GTCTCACTCT	GTTGCCCAGA
5101	CTGGAGTGCA	GTGGCGCGAT	CTCGGCTCAC	TGTAACCTTT	GGCTCCTAGG
5151	TTCAAGCAAT	TCTCCTGCCT	CAGCCTCCCA	AGTAGCTGGG	ACTGCAGGCA
5201	CGTACCACCA	TGCCCAGCTA	ATTTTTGTAT	TTTLAGTTGA	GACGGGGTTT
5251	CACCATGTTA	GCCAGGATGG	TCTCAATCTC	TTGACCTCAT	GATCCACCTG
5301	CCTTGGCCTC	CCAAAGTGTT	GGGATTACAG	GCATGAGCCA	CCATGCCTAG
5351	CCTGAGAGCC	ACATTCTTGT	TAACCACAAT	TTTCTCAGAG	TCTGCATTAG
5401	GGGTTGACAA	AGAGTGGAAG	GGAAGGACAA	AAGGATGGAG	AGGTGGATGG

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R3

5451 ACTAAGCATA TGTAGGTTCT TACCCAGGCC AGAGAAGGAT AGCTCAGCCA
 5501 CGGCAGTGGA TGCCATCTGC ACACATCGCC CTGACCCTGA AGACCTCGGA
 5551 CTGGACAGAG AGCGACTGTA CTGGGAGCTG AGCAATCTGA CAAATGGCAT
 5601 CCAGGAGCTG GGCCCCTACA CCCTGGACCG GAACAGTCTC TATGTCAATG
 5651 GTGAGCAGCT GTGATGTGGT TGGAGGCTCT TCCTCCTTGC TGAGCAGCCT
 5701 GTAATCACTG GCTTGAGGTC AACTCACTG TCAGGCAATT GAAAATTTGG
 5751 TCCTGTGCTC TACATGGGAT GACTAATTTT CGGACTTCAT GGTATCTTTT
 5801 TTTTTTTTTT TTTTTTTTTG AGATGGAGTC TCGCTCTGTC ACCAGGCTGA
 5851 GGTGCAGTGG CATGATCTCA GCTCACTGCA ACCTCCGCCT CCCGGATTCA
 5901 AGCAATTCTC CTGCCTCAGC CTCCTGAGTA GCTGGGACTA CAGGTGCATG
 5951 CCACCACACC CAGCTAATTT TTGTATTTTT AGTAGAGACA GGGTTTCACC
 6001 ATGTTGGTCA GGATGGTCTC AATCTCTTGA CCTTCTACTC CACCTTGCCCT
 6051 TGGCCTCCCA AAGTACTGGG ATTACAGGCT TGAGCCACCA CACCTGGCCA
 6101 GGACTTCATG GTTCTTCAT CATCATGGAA TGAATTCCAT CAGGGCATTC
 6151 TTCCCTGATG TGAGGGCACT GATAGGAAAT CTTTAATGGT CCCTGCTGCA
 6201 TGAAACTGCT TCCATTGCAC CAGGGTAGCC CTGACCCCTA TTTGGTCCCC
 6251 CACATCTCCT TGTAACCTAC CCACACTCCT CCCTCCTTCT CTGTGCAGGT

Exon R4

6301 TTCACCCATC GAAGCTCTAT GCCCACCACC AGCAGTGAGT ATTCAACTCA
 6351 TGTCCACATG CCCATGATCC TACACCAAGC AAAGCAGGAG CTGCCCCCTCC
 6401 TCATAAACCC ATAAGTCCTC CTCTTGAGCA AAGTAGCTGG GAAGGCAGAA
 6451 GTTATTCAAG CTCCCCCTCTG CCCCAGTTTC AAAGACAGAC TCAGCTCAAG
 6501 CCCACATGCA GCAAACCCTA TAAAAGTCTC ACCTCTTGGC ATTTCTGCCA

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

6551 TGGTAATGCT TTCTGCTCTC ACTAATGAGG ACTTCTCCTC AGCTCCTGGG

Exon R5

6601 ACCTCCACAG TGGATGTGGG AACCTCAGGG ACTCCATCCT CCAGCCCCAG

6651 CCCCACGAGT AAGTACCAGT CAATGGCATC TCTATTAGAG CATGCTATCT

6701 CTGTCATTTT TACTCAGATG AAGATGGAAA ATCATAGCAA ATCTACTGAT

6751 AGTGAGTGGA CCAACGAAAT TTGTTGGCCA CCTAGTGTGT ACCAGATCCT

6801 AGAGATACAG GAGGGAAAAC AAAACCAATA CAAAATTTCT GCTCTCAGTG

6851 AGCTTGTATT CTTGTCATGA TGATGATGTT GGTGGTGGTG CTGTTGATGA

6901 CGATGATGAT GATGATGATG ATGATGATGC TGGTGATACT GTTGATGGTG

6951 ATAGTGATGT TGATGACAAT GATGATGATG ATGATGTTGA AGAAAATGAT

7001 GCTGGTGATG GTGGTGGGGG TTATTATGGT AATAATGATA TGTTGAGTGT

7051 GACGATGATG GTGGTGGTGT TGATGATGAT GATGATTATT ATGCTAGTGA

7101 CATTGATGAT GGTAAATGGTG ATATCAACGA CAGTGACAAT GATGGTGATG

7151 AGGATGATGT CCGTGATGGT GGTGGGGTTA TGATGGTAAT GATATGTTGA

7201 ATGTGATGAT GGTGATGATG ATATTTGTGG TTCATGATGG GGATTGTCAT

7251 GGTGGTGCTG GTGGTACTTG TGATGACAAT AATGATAATA ATGATGACAA

7301 TGATAGTGAT GATGGTGATG GTGATAATAA AGATAACAGA TATCACCTTA

7351 CAATATTGAG CACTAAATAT GTACCAAGAG CTATGCTCAG TATCTAACTA

7401 CTATTATATA ATCTACTTTA GAAAATGAAT TGTATCATAG ATAAGAAAGG

Table 2 (continued)

**Genomic Repeats
(SEQ ID NO: 2)**

7451 CGTGGAAAAT ATTTATTATG TCACTCAATT TAATTGCTGC ATATGGTTAT

7501 TACAAAGTGC TATTCTCTCT ACTTTGAACA TAATGTTTAT TTCACACTCC

Exon R1

7551 CACTATAGCT GCTGGCCCTC TCCTGATGCC GTTCACCCTC AACTTCACCA

7601 TCACCAACCT GCAGTACGAG GAGGACATGC GTCGCACTGG CTCCAGGAAG

7651 TTCAACACCA TGGAGAGTGT CCTGCAGGGT CTGGTTAGTG TCCTGCCCTC

7701 CACACTCTGC CCTGCTCATG ATACCCAGTC CCTCTTACAT CATCCATGCC

7751 AGGGCAATGG AAGAATATCA AACCCAACTC ACTTTTGCCC CAAGAGATGC

7801 AAGCCTCAGC CAGGAGCGGT GGCTCACGCC TGTAATACCA GCATTTGGGA

7851 GGCCAAGGCG GGTGGATCAC CTGAGGTCAG GAGTTTGTGA CCAGCCTGGC

7901 CAACATAGTG AAACCTCATC CCTACTAAAA TACAAAAATT AGCCAAGCAT

7951 GGTGGTGCAT GCCTGTAATC CCAGCTACTT GGGAGGGTGA GGCAAGAGAA

8001 TCACTTGAAT CAAGGAGGCA GAGGTTGCAG TGAGTCAAGA TCATGCCACT

8051 TTACTCCAGC CTAGGCAAAA AAGCGAACT CCATCTCACA AAAAAAGAA

8101 AAAAAGAGAG AGATGCAAGC CTCCCCACC AAGGCCAGCC CTGCCCACCT

8151 CACTTCTGCC TGGCTCTTAC ATAAACTTA GCCCTCCTAC TCACTGCCCT

Exon R2

8201 CTCCCTCCTC CACAGCTCAA GCCCTTGTTT AAGAACACCA GTGTTGGCCC

8251 TCTGTACTCT GGCTGCAGAT TGACCTTGCT CAGGTGAGAA CTTAGAATTT

8301 CCAGCCTGGC TGCCCCACTT GTACTCACTC CAAAAGACTT TGCACTGCTT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
8351	CCTTGCTGCA	CTTCCTAGGG	ATATCCTCAC	CAAAGGTGGA	ATTCAGGAGT
8401	CACAGGCTTC	AGGATCAGTG	TGTTTCCTGA	CAGTAACACC	CCTACACTCC
8451	ACCTCAACAG	AGAGAATCTG	CATGGCCCAT	CATCAGGATT	GAGCCTCTCC
8501	CTTTATCATC	CCTCTGAATT	CCCTCCATTC	CCTGTGCCTC	CCTTTCCTTT
8551	ACATGTTAAA	TTCTGTCCCC	AGGATTTCTT	TCAGGACAAAT	CATGCCTTAT
8601	CCACGTGATT	TCATCCTCAT	TTCGAGCTCT	TCACTGGGCT	CAAGTCCGGC
8651	TCCCCGTCCC	GTCCATGAAA	GTGTCAGTTT	CATCTTGTC	CTGTATCCGT
8701	GACTCCACTC	ACAGTCCTCA	GCAAGCCAAT	AGTCCATGCA	CTAAGAGTCG
8751	ATGTGGCTTC	TCACCTCTTT	CCCAGGTTTC	TCATTTCTCT	GGTCCTTGCT
8801	GTCCTTCCCT	CAGCAATCGC	AAGACCCTTC	CTAGATAAAC	TTTTCATTGT

Exon R3

8851	GATTTTCCC	ACTGACCCTC	CCCAGGCCCG	AGAAAGATGG	GGCAGCCACT
8901	GGAGTGGATG	CCATCTGCAC	CCACCGCCTT	GACCCCAAAA	GCCCTGGACT
8951	CAACAGGGAG	CAGCTGTACT	GGGAGCTAAG	CACTGACC	AATGACATTG
9001	AAGAGCTGGG	CCCCTACACC	CTGGACAGGA	ACAGTCTCTA	TGTCAATGGT
9051	GAGTGGCTGT	GATGTGGTTG	AAATCTCTTC	CCCCTTGCTG	GGCAGCCTCT
9101	AATCTCTAAC	TAGAGATCAC	ACTCCCTGCC	TGGCCTTTGA	AAATTCTGTC
9151	ATGTGCTCTA	CATGGGATGA	CTAAGGTCTG	GACTTCATGG	TTTCCTTACC
9201	ATCATGGACT	GTGTTCCCTC	AGGGCATTCT	TTCCTGATGT	GAGGATGCTG
9251	ATAGAAAATC	TTCAATTGTC	CCTGTACCAT	GAAACTCGGT	TCATTGCACC
9301	AGGGTAGCAT	TGACCTCCAT	TTGGTCCCCC	ACCTCTCCTT	GTCTCTTACC

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R4

9351 CACTCTCCTC CCTCCTTCTC TATGCAGGTT TCACCCATCA GAGCTCTGTG
 9401 TCCACCACCA GCAGTGAGTA TTCAACTCAT ATCCACATGC CTCGGTTCCT
 9451 ACACCAAGAG GAGCAGGAGC TGGCCCCCTCC TCATAAACCC ATTAAGTCCT
 9501 CTTCATAAGC AAAGGATTTA GGAGGGCAGA AGTTATTTAA GTGTCCCTCT
 9551 GCCCAGCTCA AGAGACCGAC CCAGCTCAAG CTACACATGC AACAAACCCC
 9601 ATAAATAGTC TCCCCTCTTG CCATTTCTGC CAAGAGAGTG CTTTATGCTT

Exon R5

9651 TCACTGATGA GAACTTTTCC TCAGCTCCTG GGACCTCCAC AGTGGATCTC
 9701 AGAACCTCAG GGACTCCATC CTCCTCTCC AGCCCCACAA GTAAGTATCA
 9751 GTCAATGACA TCTCTATGAG AGCATACCTG ATTAGTGTA ACATCTCTGT
 9801 CATTTTCACT CAAATAAAGA TGGAAAATCA TAGTAAATCT AGTGATACTG
 9851 AGTGGACAAA TTTGTTTGT TGTTTTTTCT CATCCTTTTC ACTTTTTTTA
 9901 TTATACTTTA AGTTTtaggg TACATGTGCA CAATGTGCAG TTTAGTTACA
 9951 CATGTATACA TGTGCCATGC TGGTGTGCTG CACCCATTTG CTCGTCATTT
 10001 AGCATTAAAGT ATATGTCCTA TGCGATCCAA GCCCACGCGC CGCACCACGT
 10051 GCAACAGTTT CACAGATTGG ATGGTCCGAT ANNNNNNNNN NNNNNNNNNN
 10101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 10151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R1

10201 CTTCACCATC ACCAACCTGC AGTATGAGGA GGACATGCAT CGCCCTGGAT
10251 CTAGGAAGTT CAACACCACA GAGAGGGTCC TGCAGGGTCT GGTAGCACC
10301 CTGCCCTCTT CACTCTCCCC CGCCCTGGAT GCCGAGCCCC TCATACAACA
10351 TTCATGCCAG GGCAATGGAA GAATATCGCA CCAACCTTGC CCTCATCCCC
10401 AGAGATGCAA GCCTCACCCA CTGAGGCCAG CCACTCTCAT GGGTGTCTGC
10451 CCCACCCACC TCACTTTTGT CCCACACAG GGACCTTAGC CCTCCTACTT

Exon R2

10501 ACCTCTCTCT CCCTCCCCCA CAGCTTAGTC CCATATTCAA GAACACCAGT
10551 GTTGCCCCCTC TGTACTCTGG CTGCAGACTG ACCTCTCTCA GGTGAGACCT
10601 TAGAAGATCC AGCCTGGCTG CCCAGTTGT TCCCACTCCA GTAGATTTTG
10651 CTCTGCTTCC TTGCTGCACC TCCTAGGGAT ATCCTCACCA AAAGGGGAAT
10701 TCAGGAGTCA CTGGCTTCTG GACCAATGTG TTTCTGATA GTAACACTCC
10751 CACACCTCAC CTCAACAGGG AGAATCTGCA TGGTCCATCA TCAGGATTGA
10801 GCCTCTATCC TGATCATCCC TCAGAATTCC CTGCCCCCTCC CTTTCATTTA
10851 GGTGTTAAAT TCTGTCCCCA GAATTTCTCT CAAGACAATC ATGCCTCATC
10901 CAAGTGCTTT CATCCCTGTT TCTAGCTCTT CACTGGTCTC AAGTCTGGGC
10951 TCTCCTGTCC CCATGCTATG AGAATGCAGG TTTCACCTTG CACTTTTATA
11001 AGCATGGTTG TATCTGTGAC TCTGTGCACA GTCCCAAGCA AGCCAGTAGT
11051 CCATGCACTC AGAGAATCTA AGTGTAGCTT CTCACCTCTT TCCCAGGTTT
11101 CTCATTTCTT CTGGTTCTTT ACTGTCTTTC CATCAGCAGT CTCAGGACAC

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R3

11151 AACCTAAGTA ATCTTTTCAT AGTCATTCTC CCCACCTACC TTCCCAGGT
 11201 CTGAGAAGGA TGGAGCAGCC ACTGGAGTGG ATGCCATCTG CATCCATCAT
 11251 CTTGACCCCA AAAGCCCTGG ACTCAACAGA GAGCGGCTGT ACTGGGAGCT
 11301 GAGCCGACTG ACCAATGGCA TCAAAGAGCT GGGCCCCTAC ACCCTGGACA
 11351 GGAACAGTCT CTATGTCAAT GGTGAGCAGC TGTGATGTGG TTGGAGTCTT
 11401 TTCCTTCTAG AGTCTGGAAA GAATCTAATC TGTGGCTTGA AGTCACACTC
 11451 CCTGCCTGGC CATTGAATAT TCTGTCATGT GGTGTAGATG GGATGACAAA
 11501 GTTCTGGACT TCACAGTTTC TTCATTGTCG TGAAGTGTGT TCCCTCAGGG
 11551 CACTCTTCCC TGTGTGAGG ATACTGATAG GAATTCTTTA ATGGCCCCAG
 11601 TCCCATGAAA CTCATTGTCC CATGAAACTC ATTTAATTGC ATTGGGATTG
 11651 CCATGACCTT ATTGTGTCCC TCGTATCTCC TTAACGCTTA CCAAGTCTCC

Exon R4

11701 TCCCTCCTTC TCTATGCAGG TTTCACCCAT CGGACCTCTG TGCCCACCAC
 11751 CAGCAGTGAG TATTCAACTC ATGTCCACAT GCCCCTGATC CTACATTAAG
 11801 TGGAGCAGGA GCTGGCCCCCT CCTCTTAAAC CCATAAGTCC TCCTCTTGAG
 11851 CAAAGGAGCT GGAAGGCAG AAGTTATTGA AGCTCCCTTC CACCTAGCTC
 11901 CAAAGACAGG CCCAGCTCAT GCCCGTATGC AGCAGACCTC ATAATAGTCT
 11951 ACCTTCTTGC CATTTCTGCC ATGAGATTAT TTTCTGCTTT CACTGATGAG

Exon R5

12001 CACTTTTTCT CAGCTCCTGG GACCTCCACA GTGGACNNNN NNNNNNNNNN
 12051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 12101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R1

12151 ATTTTCAATT CCCACTACAG CTGCTGGCCC TCTCCTGGTG CTGTTCACCC

12201 TCAACTTCAC CATCACCAAC CTGAAGTATG AGGAGGACAT GCATCGCCCT

12251 GGCTCCAGGA AGTTCAACAC CACTGAGAGG GTCCTGCAGA CTCTGGTTAG

12301 TGCCCTTCCC TCCTCACTCT GCCCAGCCCC AGATATCCAG TCCCTTCTAC

12351 ATCATCCATG CCAGGGTGAT GAAAGAAGAT AGCAACAAC TCCCCCTTC

12401 CCCCCAAGAG ATGCAAGCCC CACCCACAGA GACCAGTCCT GCTTATTGGT

12451 GCCTGCTCCA CCCACCTCAC ATCTGCCCCG ACACACACAC ACCTTAGCCC

Exon R2

12501 CACTACTCAC CTCCCTCTCC CTCCTCTACA GCTTGGTCCT ATGTTCAAGA

12551 ACACCAGTGT TGGCCTTCTG TACTCTGGCT GCAGACTGAC CTTGCTCAGG

12601 TGAGACTTTA GAAGAGCCAG CCTGGGTGCC CAACTTGTT CCCACTCTAA

12651 AAGACTTTGC ACTGCTTCCT TGCTGCACTT CCTAGGTATA TCTTCACCAC

12701 AAGGGGAATT CAGGAGTCAT TGGCTTGAGA ACCAGTTGTT TCCTGATAGT

12751 AACACCCCCA TGCCCCAACT CAACATGCAA AATCTTCATG GTTCATCATC

12801 AGGATTGAGA CACTACCCTG ATTACCCATC TGAATTCCCT CCTTTCCTG

12851 ACCCCTCCCT TTCATTTAGG TGTTAAATTC TGTCCCAGG ATTTCTCTCA

12901 AGATAACCAT GCCTCATCCA CATACTGCA TCCGCCTTTC AAGCTCATCA

12951 CTAGTCTGAA GCTCTGGGTT CTCCTGTTCC CATGCCATGA GAATGCAGGT

13001 TTCACCTTGC ACTTTTATAA AAATTATTAT ATCCATGACT CTGCTTGCAG

13051 TCCCAGACCA AGATAGTGGT CTATGTACTC AGATAATCTA AGTGCAGATT

13101 CTCACCTCTT TCCCAGATTT CTCATTTCTT CTGGTTCCTT GATATGTTTC

13151 CCTCAGCAAT CTCAAGACAA GTCCTAGGCA ATCTTTTCAT TGTCATTCCC

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R3

13201 CCTCCTACCT TCCTCAGGTC CGAGAAGGAT GGAGCAGCCA CTGGAGTGGA
 13251 TGCCATCTGC ACCCACCCTC TTGACCCCAA AAGCCCTGGA GTGGACAGGG
 13301 AGCAGCTATA CTGGGAGCTG AGCCAGCTGA CCAATGGCAT CAAAGAGCTG
 13351 GGCCCCTACA CCCTGGACAG GAACAGTCTC TATGTCAATG GTGAGCAGCT
 13401 GTGATATGGT AGGGGTCTCT TCCTCCTGGC TGTGCAACCA TCTAATCTCT
 13451 GGCTTGGGGG CACACTCCCT GCCTGGCCAT TGAAAATTCT GTCACGTGCT
 13501 CTACATGGGA TGACTAAGTT CTGGACTTCA TGGTTTCTTT GTTATCATGA
 13551 GAGGCATTCC CTCTGGGCAC TCTTCCCTGT TGTGAGGATG CTGATAGGAA
 13601 ATCTTTAATG ACCCCTGTCC CATGAAACTC ATTTAATTGC ACCAGGGTAG
 13651 TCCTGAACTC TATCGCGTCC CCCACATCTC CTTAACCCCTT ACCCAGTCTC

Exon R4

13701 CTCCCTCCTT CTCTATGCAG GTTTCACCCA TTGGATCCCT GTGCCCACCA
 13751 GCAGCAGTGA GTATTCAACT CATGTCCATG ATGCCCCTGA TCCTACATCA
 13801 AGTGGAGCAA GAGCTGGCCC CTCCTCTTTA ACCCATAAGT CTCCTCTTGT
 13851 AGCAAATGAG CTGGGAAGGC AGAAGTTACT CAAGCTCCCC TCTGCCCCAG
 13901 CTCCAAAGAC AGACCCAGCT CAAGCCCACA TGCAGCAGAC CTCATAATAG
 13951 TCTATCTTCT TGCCATTTCT GCCATGAGAG TGCTTTCTGC TTTCAGTGAT

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R5

14001 GAGGACTTTT TTCAGCTCCT GGGACCTCCA CAGTGGACCT TGGGTCAGGG
14051 ACTCCATCCT CCCTCCCCAG CCCACAAGT AAGTACCAGC CAATGGTATC
14101 TGTATTAGAT CATGCCTGAT GAATGCAAAC ATCTGTGCCA TTTTCAGTCA
14151 AATGAAAATG GAAAATCATA ATAAATCTAG TGATACTGAG TGAACCAAAA
14201 AAAATGTATT GGCCACCTAC AGTGTACCAG ACCCTAGGGA TATAGCAAGG
14251 AAAATAGAAC CAATAAAAAC ATCTCTGCCC TCAGTGAGCT TGTGTTTCATG
14301 TGATGATATG ATGGTGGTGG TGGTGGTAAT AGTAATAATG ACATATTCAG
14351 TTTGATGATA ATTTATGATT ATGGTGTTCG TGTGATGAT GGTGGTGGTG
14401 ATGTTACTGA CAATGATGGT GACGGATCTT TGAGGATATT GTCCGTGATG
14451 GTCGTGAAGA TTATGATGAT AATGATGATG TGTAAAGTGT GATGATGATG
14501 ATGATCTGTG GTGATGCTGT TTAGGATGCT GTTCCGTGGT ACCGATGATA
14551 TTGATGTTGG TCGTGGTTAT GTTGTATGAC AATGACAATG ATGGTGATGA
14601 GGATAATCGC CAGTGATGGT GTGGGTTTAT GATGATGATG ATGTGTTGAA
14651 TGTGGTGATG ATAATGTTCG TGGTGGTCGT GATGGGCATT ACTATGGCAG
14701 TGATGGTCAT AATAATGATG GTGATGGTGA CAATGATAGC AAGGATGATG
14751 ATGGCAATAA AGATAGTACA TAACATCAGA CAATATTGAG CTCTGAATAT
14801 GCACCACGAG GAGTGCTCAG CATCTAAATA CTATTATATA ATATATTTTT
14851 GTAAAAATAA ATTGTATTGT TTTAGGCAAG GGAAGCATGG TAAATATTTT
14901 GTCACTCAAT TTAAATTCTG CATATGTTTA AAGATAAGTC TATTGCAAAC
14951 TCCTATTTTC TCTACTTTGG ACATAGTGTT TGTTTCCCAC CTCCACTACA

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R1

15001 GCTGCTGGCC CTCTCCTGGT GCCATTCACC CTCAACTTCA CCATCACCAA
 15051 CCTGCAGTAC GAGGAGGACA TGCATCACCC AGGCTCCAGG AAGTTCAACA
 15101 CCACGGAGCG GGTCTGTCAG GGTCTGGTTA GTGCTCCACC CTCCTCACTC
 15151 CGCCCCACCC CAGAGAGTCA GTACCTCCTA CATCATCCAT GCCAGGTGAT
 15201 GGAACAAGAT CATACCCACC TCACCCTTGC CCCAAGAGAT GCAAGCCATG
 15251 CCCATTGAAA CCAGCCCCAC TCACTGATGC CTGTTACTGC CCCACCTGAC
 15301 TTCTGCCCTA CACACCCACA CACGCAACTT AGCCCTCCTA CTCATCTCCT

Exon R2

15351 TCTCCCTCCT CCACAGCTTG GTCCCATGTT CAAGAACACC AGTGTCGGCC
 15401 TTCTGTACTC TGGCTGCAGA CTGACCTTGC TCAGGTGAGA CTTAGAAGA
 15451 TCAAGCTTGG CTGCCCCACT TGTNNNNNNN NNNNNNNNNN NNNNNNNNNN
 15501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 15551 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Exon R1

15601 NGTGTTAGTC TACTTTTGAA CACTGTTTAT TTCCCATCTT CACTATAGCC
 15651 GCCAGCCCTC TCCTGGTGCT ATTCACAATT AACTTCACCA TCACTAACCT
 15701 GCGGTATGAG GAGAACATGC ATCAGCCTGG CTCTAGAAAG TTTAACACCA
 15751 CGGAGAGAGT CCTTCAGGGT CTGGTAAGAG CCCCACATAC CTCATTCTAC
 15801 CGCCACTCAC CATGTTTGTAGT CCTGCCCACC TCACCTATTG CAGAGCATGG
 15851 AAGATCTCAT CTACCTCATC TTGCCCCCAG ATATGCATAC CCCAACCCT
 15901 GATGCCAGCC CCACCAACTG TTGCCAGCCC TGCCACCTC CTTCTACCA
 15951 CACCCTATG ACTTCAGTCC TCCCACTCAC CTCCCTCTCC CTCCTCCACA

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R2

16001 GCTCAGGCCT GTGTTCAAGA ACACCAGTGT TGGCCCTCTG TACTCTGGCT
 16051 GCAGACTGAC CTTGCTCAGG TGAGAACTGA GAACAGCCAG TCTGACTGAT
 16101 CTGAGCAGTT TGACCTGCTT CCCTTCTGCA CTCCCTGGAG ATGTCCGCAG
 16151 CCAGGTGGAA TCCAGGAGGC AGTGGCTCTA AGACCAATGT GCTTCCTGTT
 16201 CCCACCACCT CCCACCTCAA CTGAGAGATG CAGAGCCCAT CAGCAGGACT
 16251 GAGCTTCTAC CTTGGTCATC CCTCTGAATT CCCTCCTTTC CCCTACCTGC
 16301 CTTTCCACAA GTGGTTCAAT TCTGTTCCCA GGATTTCTCC CAAGAAAAAC
 16351 ATGCCTCGTC CACTTGCTTT CATCCCCAAA CCTAGCTCTT CACCTGTCTC
 16401 AAGTATGAGT TCTCCTTACC CCATGCTACA AGAATGCAGT TTCCACTTTG
 16451 CAATTTTATA AAAATCCTTG CATCCATGAT TCTGCTCATA GTTGCTAAGA
 16501 GTCAGTGCAC TCAGAGAATG GAAGTATGGC TTCTCACTTC TCTACCAGGC
 16551 TTCTCATTTT CTCTGGCCCC CTCCTGTCCT GCCCTGTGGG ATCTCAGAAC
 16601 CCCTCCCTAG GCAATCCGTG TATTGTCTTT CC CAATCTT GCCCTCCCCA

Exon R3

16651 GGCCCAAGAA GGATGGGGCA GCCACCAAAG TGGATGCCAT CTGCACTTAC
 16701 CGCCCTGATC CCAAAGCCC TGGACTGGAC AGAGAGCAGC TATACTGGGA
 16751 GCTGAGCCAG CTGACCCACA GCATCACTGA GCTGGGCCCC TACACACTGG
 16801 ACAGGGACAG TCTCTATGTC AATGGTGAGT AGTTGTGATG TGGTTGGAGT
 16851 CTCTTCCTCC TTGCTGGGCA GCCTCTACTC TCTGCCTTGA GGTCACGCTC
 16901 CCTGCCTGGC TATTGAATGC TCATCCATGT TGTCTGTATG TGATGGCTGA

Table 2 (continued)

**Genomic Repeats
(SEQ ID NO: 2)**

16951 GGTGGAAC TCAATGGTTTC TATTTTCATCT TGGACTGAGT TCATCCTCAG
 17001 GATCTGCTTT CTGGATCTGA GGGTGCTGAT AGAGAATCTT CAATGGTTCG
 17051 TGTTCCTGGA AATTCCTTCC ATTGCACCAG GGTACCCTGA CCCCTATATA
 17101 GTTCCCCACC ACTCCCTTAA CCCTTACCCA CCCTCTTCCC TCCCTCTCTA

Exon R4

17151 TGCAGGTTC ACACAGCGGA GCTCTGTGCC CACCACTAGC AGTGAGTATC
 17201 CACTGATTTT CAGTGCTCCT GATCCTACAT CATGCAGGGC AAGAACTGAC
 17251 CCCTCCTCAC ATGCCCCTAT GTCTCTATG AGCAAAGGAG CTGGGACAGC
 17301 ACAAGTTACT CCCTTTCCCT TCTGGCCCAA GTCTCTTCAG AGAGAGACCC
 17351 AGCTCAAGCC CCACATGCAG CAAGGTCCAT AAATACTCCT ACCTGCTGGC
 17401 ATTTCTGCCA TGAGAGGGTT CAACACTTTC ACTAATGAGG CCTTCTCCTC

Exon R5

17451 AGTTCCTGGG ACCCCACAG TGGACCTGGG AACATCTGGG ACTCCAGTTT
 17501 CTAAACCTGG TCCCTCGGGT AAGTACAAAT CAATCGCATC TCTGTTAGAG
 17551 CATGCCTGAT GACTGTCAAC ATCTCTGCCA TTTTCACTTA AATAAAGATA
 17601 AAAAATCCTA GTGAATCTAC GGATGAGGAG TCATCCAGCA AACTTAATTG
 17651 AGTGCCTAGT TTCTGCAGGG CTCTAGGGAT AAGAAAGGGG ACACAAAACA
 17701 GTTAAAAATA TCTGCTGCAA GAAAGCTTAT TTTATTGTGA GGGTGATGGG
 17751 AGTTGGTGGT GGTGAAGTTA CTGGAGATGA TGACAATAAG AATGGTGATG
 17801 CTAGTGATGA TGATGGTGAT AAGGATGATA ATTATGAAGA TGGTGGTGGT
 17851 GATGATGATG ATGGTNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 17901 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 17951 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 18001 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Table 2 (continued)

**Genomic Repeats
(SEQ ID NO: 2)**

18051 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18151 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18401 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Exon R1

18501 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NGCTGCCAGC CCTCTCCTGG

18551 TGCTATTCAC TCTCAACTTC ACCATCACCA ACCTGCGGTA TGAGGAGAAC

18601 ATGCAGCACC CTGGCTCCAG GAAGTTCAAC ACCACGGAGA GGGTCCTTCA

18651 GGGCCTGNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18701 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18751 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

18801 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Exon R2

18851 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNCTC AGGTCCCTGT

18901 TCAAGAGCAC CAGTGTGGC CCTCTGTACT CTGGCTGCAG ACTGACTTTG

18951 CTCAGGNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNAGAA

19001 TCAGTCGACC TACCGGCTTT GATGATTGCT CAGTTGAACT TAGAAATGCA

19051 CTGTCTGCCC AATGGTCCAG TCTCATGAGT GTGACTCTTT TCTGCCTCTC

19101 TTGGGTATCT GATCAAGATG GACTCAGGAA AAGTGCTCCA GATAACTGTC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
19151	TCCAATATAA	CACTGCCCCCT	GCCATCACAC	CCAAATGACT	GGAAGTTTCA
19201	CAGGGTCATC	AGCAGGGATT	GGACTTCCAC	CCCGGCCATC	CCTCTGAATT
19251	TTCCCTCTTT	TCTCCCCACC	TCCCTTGCCC	TTAGGTGTTA	AAATTCTCTA
19301	ACTAAGATTT	CTCTCAAGAC	AAATGTGCCT	CATTCACCTG	TTTAATTCCC
19351	AATTCAGCT	TGTCACCTGT	CTCAAGTCTA	GGCTGTCCTG	TCCCCATGCC
19401	ATGAGAATGC	AAGAACCACA	CTGAAATGTT	AGAAAAATTC	TTTTATCCAC
19451	AAGTATGCTC	ACCGTCCCAA	GCTGGACAGT	AGTCAGTGCA	CTCAGAGAAT
19501	CTAAGTGTGG	CTTCTCATCT	GTGTACCAGG	CTTCTCATTT	CCTGTGGGCC
19551	CTTCTTGTC	TTCCCTCCGC	AATCTTGGA	CTCCTCCCTA	GACAAAACCT
Exon R3					
19601	TATTATTATT	CCCCTCACCT	GCCCTCTCCA	<u>GGCCTGAAAA</u>	<u>GGATGGGACA</u>
19651	<u>GCCACTGGAG</u>	<u>TGGATGCCAT</u>	<u>CTGCACCCAC</u>	<u>CACCCTGACC</u>	<u>CCAAAAGCCC</u>
19701	<u>TAGGCTGGAC</u>	<u>AGAGAGCAGC</u>	<u>TGTATTGGGA</u>	<u>GCTGAGCCAG</u>	<u>CTGACCCACA</u>
19751	<u>ATATCACTGA</u>	<u>GCTGGGCCCC</u>	<u>TATGCCCTGG</u>	<u>ACAACGACAG</u>	<u>CCTCTTTGTC</u>
19801	<u>AATGGTGAGC</u>	<u>AATTGTGATG</u>	<u>TGGTTGGAGT</u>	<u>TTCTTCTTCC</u>	<u>TTGCTGAGCA</u>
19851	GGCCTCTACT	CTCTGTCTTG	AGGTCACCT	CCCTGCCTGG	CCACTGGTCT
19901	TGGCCATGTT	GTCTGTATTT	GATGATTGAT	ATGAACTTCA	CCGTTTCTTC
19951	TTCATCTTGT	ACTGGAGACC	TTCATCCTCA	GGACCTTCTT	CCCTGATCTG
20001	AGTGTACTTG	TATAGAATCC	TCAAAGCCCA	TGTTCCCTGA	AACTCCTTCA
20051	ATTGCACCAT	GGTAGCACTG	ACCCCTTTTG	GTCCCCCACC	TTNNNNNNNN

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R4

20101 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN TTCACTCATC

20151 GGAGCTCTGT GTCCACCACC AGCACTNNNN NNNNNNNNNN NNNNNNNNNN

20201 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

20251 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

20301 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN

Exon R5

20351 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNCCTG GGACCCCCAC

20401 AGTGTATCTG GGAGCATCTA AGACTCCAGC CTCGATATTT GGCCCTTCAN

20451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNGACTCCA GCCTCGATAT

20501 TTGGCCCTTC AGGTAAGTAC CAGTCAATGG CACCTCTATT AGAGTATGCA

20551 TGATGAGTGT CAACATCTCT GTCCTTTTCA CTCAAATAAG ATTAAAAATC

20601 ATAGCAAATT GTACGTGATG ATGAGTCACC CAACAACTT CTTTGAGTAC

20651 CCACTCTCTG CCAGGCCCTA GAGATAAGGC AGGGAACACA AAAGAGGTAA

20701 AAATCTCTGC CCTCAGAGAG CTTCTTTTAT TTTGAGGATG ATGTGGGATA

20751 GTGGTGATGA TGATGTTGCT GGAGATGATT ACAATAATGA TGGTGATGCT

20801 TATGACCATG ATGTGATGAT GATGGTGATT ATGAAGATGA TGATGATGAT

20851 ATTGATGATG GTAGTGGTTT TGACAGTAAT GATGATGTGA TGATGATGAT

20901 GATAGTGGTG GTGGTGATTA TGGGAAGGAT GACAGTGGTG GTGGTGATGG

20951 TGGTGGTTGT GGTGGTGATT GACAATGTGG TGGTGATATT GACAATGAGG

21001 ATGATGATGA TAGTGGTGGT GGTATGATG GTTAAGGATG ATGTGATGAT

Table 2 (continued)

		Genomic Repeats (SEQ ID NO: 2)					
21051	GGTGTGGTG	ATCACGGTAC	TAGTGGTGGT	GATGTGGACC	GTCATGGTTG		
21101	TGGTTGTGGT	GGTGATGGTG	GTGATCATGA	TGATAATGAG	GATGATGGTG		
21151	GTGATTGTCA	TGATGGTAAG	GATGAAACAG	TGATGGTGTT	GGTGACCATG		
21201	TTCCTGGTGG	TGATGGTGCA	GGTGATGATG	TGGATGATGA	TGGTGATGGT		
21251	GGTGGAGATG	ATAGGGATTA	TGAATATGGT	TCGGGTCTCT	GA CTGGTGGT		
21301	GGTGATGACA	ATAATGAAAA	TGATGGTCAC	AGTGTGGTG	ATGATGATGG		
21351	TGGTGATAAC	AAAGGTAATA	GATAGTGTCT	AGTATTATGG	AACACAGAAC		
21401	ATCACCAAAG	GTTATGCTCA	GCATCTAACT	ATTATTATTT	AGCATGCTCT		
21451	ATGAAAAACT	TTGATCGTTA	TAGTCAAGGG	AGGCATGAAA	ACCTTCTATT		
21501	TTATCACTCT	CTTTAAATCT	GGTTGCATAT	GTTTAGAAAT	AAATCTATTA		
21551	CAAACCTCTTA	AATGTTCTCT	ACTTTTGAAC	ATAGTGTTTA	TTTCCACCT		
Exon R1							
21601	CCACTACAGC	TGCCAGCCAT	CTCCTGATAC	TATTCACCCT	CAACTTCACC		
21651	<u>ATCACTAACC</u>	<u>TGCGGTATGA</u>	<u>GGAGAACATG</u>	<u>TGGCCTGGCT</u>	<u>CCAGGAAGTT</u>		
21701	<u>CAACACTACA</u>	<u>GAGAGGGTCC</u>	<u>TTCAGGGCCT</u>	<u>GGTGAGAGCC</u>	<u>CTGCCCACCT</u>		
21751	CACTCTGCCC	TGCCCACCTT	GTCTTGTTCC	ACCTACGTCA	CCCATTCCAA		
21801	GGCATGGAAG	AAGATCTCAC	CCACCTCCCC	TCACCTGAGA	GATAGCCCCG		
21851	CCCCCTGATT	ACAGCCCCTT	CCACCTTACA	TCTTCCTCAC	TTCTATGTCC		

Table 2 (continued)

Genomic Repeats
(SEQ ID NO: 2)

Exon R2

21901 TCAGCCATCT TACTCACCTC CCTCTTCCTC CTCCACAGGC TAAGGCCCTT

21951 GTTCAAGAAC ACCAGTGTG GCCCTCTGTA CTCTGGCTGC AGGCTGACCT

22001 TGCTCAGGTG AGAACTGAGA ATAACCAGTC TGGCTACCCC AAGTGTTCCT

22051 AGGCCCCAAGG AGTTTCATCA GCTTTCTTCC TTCCCTCCCT ATGGAAGTCC

22101 TCAGCACAAG TGAATTTCAG GCGTTGGTGG CTCCAGGATG AACATATCTG

22151 CTGATCCTAC CACCTCCCCC ATCAATCGAG AGAATTTGCA GGGCCCATCA

22201 GCCAGATCAG GCTTCTACTT TGGTCATCCT TCTGAATTTC TTAATTCTCC

22251 CTACCTCCCT CTCCTTCAGG TGTAAATTC TCTTCCAAGG TTTCTCTCAA

22301 GATAAACATC CCCCATCCAC TTGCTTTCAT CCCCATTCC AGCTCTTAAT

22351 ATTTCTCAAG TCTGGGCTCT CCTGTCCCCA TACCATGAGA ATGCAATTTT

22401 ATAAAATTCT TGTATTCTTG ACTCTACTCA CATTCCCAGG CTGCCTGGAA

22451 GTTGGTGCAT TCAGAGAATC TTAGTATGGC TTCTCACCTG TCTACCAGGA

22501 TTCTCATTTT CTCTGTCCCC TTCCTGTCCT GCCCCCAGGA ATCTCAGGAT

22551 GCCTCCCCAT AGGCAATCTA TTTAATGTCA TCCCCCTTAT CTGCCCTCCC

Exon R3

22601 TAGGCCAGAG AAAGATGGGG AAGCCACCGG AGTGGATGCC ATCTGCACCC

22651 ACCGCCCTGA CCCCACAGGC CCTGGGCTGG ACAGAGAGCA GCTGTATTTG

22701 GAGCTGAGCC AGCTGACCCA CAGCATCACT GAGCTGGGCC CCTACACACT

22751 GGACAGGGAC AGTCTCTATG TCAATGGTGA GCGGCTGTGA TGTGGTTGGA

22801 GATTCTTCCT CTTTGCTGGA CAGCTTCTTA CTCTCTGACT TGAGGTCACA

22851 CTCCCTGACT GGCCATTGAC GTCTTGCTTA TGTGTCTGT ATGTGATGAC

22901 TGATGTCTGA ACTTCATAGT TTCTTCATCT TGGACTGAGT TCATCCTCAG

22951 TACCTTCTTC CCTGATCTGA GGGTACTGAT AGAGAATCTT CAAAGGCCCC

Table 2 (continued)

		Genomic Repeats (SEQ ID NO: 2)					
23001	TGTTCCCTTGA	AACTTCTTCC	ATTCCACTAG	GGTATCTGTG	ACCCCTATTT		
23051	GATTCCCCAC	CTCTCCCTTA	ACCCTTACCC	ACTCTCCTCC	CTCCTTCTCT		
Exon R4							
23101	GTGCAGGTTT	CACCCATCGG	AGCTCTGTAC	CCACCACCAG	CAGTGAGTAT		
23151	TCAACCGATG	CTCCAGTAGC	CCCAATTATA	CACCAAGCAG	GGCAGGAGCT		
23201	GTCCTGTCTT	CCTATGCCCC	TATGTCCTCT	TCATAAAGGA	AGGGGCTGGG		
23251	AGGGCACAAAG	TTATTCCCTT	TCCCTTCTGG	CCAGCTCCAG	AGAGAGACCC		
23301	AGCTCAGGCC	CGATATGCAG	CAAGGCCTGT	AAATAGTTTT	ATTTGCTGAC		
23351	CTTTCTGCCA	TGAGAGGCTT	GGATGCTTCC	CCTGAAGAGG	GTTTCTCTGT		
23401	AGCTCTTGGG	ACTACCACAG	TGGACCTGGG	AAACTCTGGG	GATCCACCCC		
23451	TTCTACTGGT	CCCTTGAATA	AGTACCAGCC	AATGGCACCT	CTGTTAGAGC		
23501	ATGGCTGATG	AGTGTAACA	TCTCTTCCAT	TATTCAGTCA	AATAAAGATG		
23551	GAAATTCTTT	ATAAATCTAG	TGATGATGAG	CCAACCAACA	AACTTTATTG		
23601	AGCATTGTGA	CAAGCCCTGG	GGCTCTGCCA	AATCCTGGGG	ATATGGCATG		
23651	GATCATGAAA	CAATTAATAA	TCTCTCCTCT	CAGAGAGCTA	TTTTTATGAT		
23701	GATACTGATG	GTGGCAATGA	TGATGATGTT	GATGGTGATT	ATGACCATGA		
23751	TGACAATGGT	GATGGTGGTG	GTGATGATGG	TAATGATGAT	GATGGTGATG		
23801	TTGGTAATGA	TGGTGGTGAT	TATGACAATA	ATGATGGTGA	TGGTGACAGG		
23851	GATGGTGATG	ATTATGATGG	TGGTGGTGAT	AACAAAGTTA	ATGGATAATA		
23901	TATGAACTTA	TTGGCTACTG	AATATGCACC	AAAGTGCTAT	GCTCAGTGTT		
23951	TAACTAGTAC	TATTTAATAT	GATTTCATAA	AAAAATCTTG	AATTATTATA		
24001	GGCAGAAGAA	TCATGGGAAC	CTTTTATTTT	GTCACCTACT	TTAAGTCCTA		
24051	TTGCATATTT	TTTAAGTCAA	TTGCAAACAC	AGTTTCTCTG	CTTTGAACAT		

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
24101	TGTGTTTATA	TCCAGTCACC	CCAATAGTGC	ATAAACCTGC	TGATTGGAGC
24151	AACTGTGTCT	TACTCCCTTG	TGCTTCCCTA	GTATCTGCTT	CAGGACCTTG
24201	TACATGGTAG	ATCGACAGAT	TTAGATCTAC	AGGAAAATAT	GGATTTTCCC
24251	AGGGAAGGAA	GGAATGAAGT	ATGCTTTCTT	ATAATGTATG	GAAACTTTCC
24301	TCTTCTGCCT	TGGTTCAACT	TTAGTGTCTG	CCAGAGTTTA	CACTGGAAAA
24351	CTATATGGCA	TCTGCTCCAC	TCCCTCATCC	ATGACAGACA	TCATTAATTG
24401	ATTGCAGCAT	TCATGGCAGA	CATCACCAAT	TGATAATAGC	ATTCATTTTC
24451	TCTCAGTTCA	AAACAGCTTC	AGAATGGTTA	CCAAAAA	AAAATTCAGT
24501	CGCTACCAAT	TCAATTGGAG	CTGACTCAGG	ATTATGGGAC	AGAATTCAAG
24551	AGAGTTAGGT	TCCTTGATGA	TGTGTAGTGG	CTATTGTGTT	TCCGGTCCAG
24601	GCTAATNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
24651	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
24701	CTTTGTGCGG	CAAAGTTCAG	GGGCCCAAA	AATTTCTGTG	CCCAATCAT
24751	GGCGGACCTA	GGTTTAGGCA	CAAATCCAG	GCATTAAGTC	CCTGGAGATG
24801	TTATGGCTTT	TGGTTTTCTT	AGAAAGGCTC	AGCTCAGGCT	CAGCTTGGTC
24851	ATGCTGATAT	CCTTTCTTCC	ACTTGGTCGA	TTTGGCTGTT	GATACTTATG
24901	TATGCTTCAC	GAAGTTTTTG	TGCTGTGTTT	TTCAGCTCCA	TCGGTTGGTT
24951	TATGTTCTC	TCTAAACTGG	TTATTCTAGT	TAGCAATTCC	TTTAACCTTT
25001	CATCAAGGTG	CTTAGCTTTG	CATTGCATTA	GAACATGCTC	CTTTAGCTCA
25051	TCGTACTTTT	TTATTGCCCA	TCTTCTGAAG	CCTACTTCTG	TCAATTCATC
25101	CATCTGATCC	TCCATCCAGT	TCTGCACCCT	TAATGGAGAG	ATGTTGCGGT
25151	CATTTGGAGG	AAAAGAGGCA	CTCTGGCCTT	TTGGGTTTTT	AGCATTTTTT
25201	TGTTGATTAT	TTCCCATCTT	CAGGAGTTTT	AGTTTCAGGC	TTTGAGGCTG
25251	CTGATCCTTG	GATGGGGTTT	TTATGGGGGT	CTTTTGGTTG	TTGTTGTGA

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
25301	TGATGATGAT	GTTATTGTCA	CTTTCTGCTT	GTTTTTCTTT	CAATAGTCAG
25351	GTCCCTCTTC	TGTAGGGCTG	CTGCAGTTTG	CTAGGGGTTC	ACTTCAGGCC
25401	CTATTCATCT	GATTCGCTCC	CATGTCTGGA	GGTGTCACTC	AAGGAGGCTT
25451	GGAGAGCAGC	GAACATAGGT	GCCTGCTTCT	TCTGGGACCT	CTGACCTCGA
25501	GGGACACCAA	CCTGATGCCA	GTAGGATCGC	TCCTGTGTAG	GGTGTCTGAC
25551	AACTATTGTT	GGAGGGTTTC	GCCCAGTTGA	CTGGCATGGA	GAGCAGGACC
25601	CATTTAATGA	AGCACTTTGT	CCCCTGGTGG	AGAGGGGGTT	CTTCACTGGG
25651	GGGAAACCAC	ATGTCTGGGC	TGCTTGGATT	CCTCAGAACT	ACCAGAGGAG
25701	AGGCTAAGTC	TGCTGGTCCA	CAGAGACTAC	AGCCATCCCT	CCCACTAGGG
25751	GCCCAAGCCC	AGGGAGTCCA	AATTCTGTCT	CTGAGCCTCT	GGCTGGAGTC
25801	TTTGGAGATC	CTGCAAGGAA	GCTCTGCCCA	CTGAGGAAGG	ATGGGTGAGG
25851	GTTAGCCCTG	AAGAGGCACT	CTGGCTGCAG	ACTGCCACAG	CCGGTGTGTT
25901	GGGCTGTGGG	GACAAGTCTT	GGGACCAAGC	CGTCCAGCCT	ACCCGGCTCT
25951	AGCAGGGGAA	AAGTACAGCC	TGGAGCTATT	GAAAGGGGTG	CCGCCCTTCC
26001	CCCGCCCAGG	GAGCTTAGCG	TGTTAGGCAG	TTGTGAGTCC	AGTGCTGGCT
26051	GTCGCCCCCTT	CCCCAAGGAA	CAAAAAGAC	TTAGCAGGCA	GCCGCAGCCA
26101	GTGCTGGTCG	CCCCTCCCCC	GGGGAGTTCC	GTAGGCTTAG	GCAGATTCCA
26151	GCTGTAAGAA	TCTGCGTGTT	CTGGGGTTGG	GACACTAGGT	CCCAGTGGCA
26201	TGGGTTCGCG	AGTGAGATCT	TCCAATCTGT	GAGTTGCACA	GTTCCGTGGA
26251	AAAAGCACAG	TTTCCCCCTC	TTGGGTAGCC	CGCTCACTCA	CCACCTCCCT
26301	TGGCTGGAAG	GAGGGGGTTC	CCCTTCCCCG	TGTGTCTCTC	AGGTGGGCCA
26351	CCACACCACA	CTGCTCTTCC	TTCTCTCTGT	GGGTCAGTGC	CAGCCTTCTA

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
26401	GTCAATTTTG	ATGAGGGAAC	CTGGACATT	TGGTTGCCAG	GAAGGATCAC
26451	ACACTTATTA	CAGTTTTTTTT	CAATGTGAGC	CTCTGAGCGC	TGCTGCTTAT
26501	AGTCGACCAT	CTTGGCCCCC	AGAGTCACAC	ATCTGTTATT	TTTTGATGTT
26551	TTGATTGTGG	CAATTCCTGC	AGAAGTAAGG	TGGTATCACC	TTATGGTTTT
26601	GATTTCCCTG	GTCATTAGTG	ATGTTGAACA	TTTTTTTCAT	ATGTTCATT
26651	GCCATTTGTA	TATATTCTTT	CAACAACTGT	CTATTTATGT	CCTTAGCCCA
26701	CTTTTTGATG	GGATTGTTTT	TTTCTTGCCA	ATTTGTTTGA	GTTTCGTTGTA
26751	GATTCTAGAT	ATTAGTCCTT	TGTTGGATAT	ATAGATTGTG	AAGATTTTCT
26801	CCCACTCTGT	GGGTTGTCTG	TTACTCTAC	TGACTGTGAA	GGAAAAGTCA
26851	ATTTCTTATA	CGAATTTGTC	TCACTCCTAC	TTCCAAATGA	GATCCTGGGG
26901	TTTTTTTTTT	CTGTTAATCC	TTCACAATAC	TTCTCCCACT	TTTTTGA
26951	CATTTGTTTA	TATTCTGTTG	TCTGCTTCTC	TTTTATAGGA	ATGTGACTTC
27001	TTATGGGCTT	TCTCTATTAT	ACCACATATG	GGTTTTTGTT	TTGTTTTGTT
27051	TTGTTTTGTT	TTGTTTTTGT	CCTCGGATCC	ATTCTCCAAC	CTCCTCCAGC
27101	CTTCCCGTGC	TCTGTGGGAT	AGACGTCTGA	CTCATGAAAA	CTACATTTCC
27151	CAGGCTCCCA	TGCTAACTAG	CTTCCTGTTA	GGTTCAGCCA	ATAGGAGGCA
27201	TTGGTGGGAC	AATGGTGGGC	GGGGCTATGG	AAGGGCCAGA	GTATTTCTGT
27251	ACCCCGCCCC	CCTGCTCCCC	TTCCAATGTT	CCTGGAGCGG	TGTAGGACCA
27301	ATACTGTATA	TATGGAAGGA	AGGCAAGGTG	GATAGATTGG	AAGGAAGAAG
27351	TGACAGATGG	AAAGAAGAAG	TGATAAATGG	CAAGCGAGGC	AAGGGAGCAG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
27401	AGGATGGATG	AGTGGATTGC	AAGAAAGAAA	AAAATGGATG	AAATATAAAA
27451	GGAGCAGGAC	AGATGGATAA	GTAGATGGAA	GTAAGAAAAG	ACTGGTGTAA
27501	GAAAGGAACG	ATTGATGATG	GATGATGAAT	GGATCAGTGG	TGATTGGGTG
27551	AAGGGATGAA	TGGATGGATG	GACAGATGGA	TGAACAGATG	GGTGGGTGGA
27601	TAGATGGATG	GATGGATAAA	ATGGGTAGGT	GGATGGATGG	ATGGATGGAC
27651	AGATGGGTGG	GTAGGTGGAT	GGATGGATAG	ATGGATGGAT	AAGTGAATGG
27701	ATGGATGGAT	GGATGGATGG	ATAAATGGAT	GGATGGGTGA	AAGGAAGGAA
27751	AGAAGTGAGA	GAAGGAAGAG	GAAGGATAGA	CAGATGTTAG	AAGGTACAAA
27801	TGAAAGGAAG	GAAGCCAGCA	AGAAAGAAAG	GATGCATTAA	TAGAATGAAA
27851	GATGGAAGGG	AAGAAGAAA	GATGGAAAGA	GAGAAGGAAG	AATGAACAGA
27901	AGGAAGTTCA	AGAGTGGTGA	AAAGAAGAAA	GGCAGGGAGA	GAAGGAGAAG
27951	TAAACTTTTC	TTCTAGAGAT	TTGTCTTAAA	CCTTAGCTTG	GCTGGACACT
28001	GTGGTTCACG	CCTGTAATCC	CAGCACTTTG	GGAGGCCGAG	GCGGGTGGAT
28051	CATGAGGTCA	GGAGATCAAG	ACCATCCTGG	CTAACACGGT	GAAACCCTGT
28101	CTCTACTAAA	AATACAAAAA	AAATTTAGTC	AGGTGTGGTG	GTGCATGCCT
28151	GTGGTCCCAG	CTACTCAGGA	GGCTGAGGCA	GGAGAATGGC	ATAAAACCTG
28201	GGAGGCAGAG	CTTGCACTGA	GCCAAGATCA	CACCACTGCA	CTCTAGCCTG
28251	GGCGACAAAG	TGAGACTCTG	TCTCAAACAA	AAACAAAACA	AAAAAACAAA
28301	AACAAAAAAC	AAAACCAAAC	CAAAACAAAA	AAAAAACCT	TAATCATAC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
28351	TTTCATAAAG	TTCCACACAC	AGGGAGTGAT	TAGAAAGCAT	TTGCTGATAT
28401	ATTTTATATA	ATAAACATGT	ACACCATATT	GACCTGTGTG	CCCAGCAGTG
28451	CTTACATGAT	TTACAATGAT	TAACTTGTTT	AAGCTTCATA	ACAACGGTTG
28501	AGGCAGGAAA	CATCATTGTG	AACCATTGTC	ATCTCATTTT	ACAGATGAGT
28551	AAACTGAAGT	GCTGAGAGGT	TGGTTATGGC	TGCAAAGATT	GTTGGCCATG
28601	TTAACCAATG	CATAGAAGAT	TAGCATACCT	GGTTGTGAGT	GCAGGAGAGA
28651	GAGAGAAATG	GGAGAAAGGC	AGAGAAGGAT	CGATGGGGAG	AGAGGAAGAG
28701	AGAGAGAGAG	AATAAATTTT	TTAAAAATGT	CTAGAGTCAT	GACTTCCGCA
28751	TCAGTGTGGT	AATATGCAGC	CTTTACCCTG	GGAAAGATCA	GAACCATTGG
28801	TACTTTTAC	AGAATCTTCC	CTTCCTGCAT	TTGGGTAGAA	GGACCCCATC
28851	TGGACATCCC	AAATCATTAA	GCACACCCTT	ACTGGCTGCT	GGAGTTGTCT
28901	CCATTAAAAG	TCACCGTTGG	GTTTATTAAG	AGGCGGACAC	AGGGTCCTTA
28951	GAACACACTG	CCCCCACCTG	TCCCACACCA	CCCCCACCC	ACCCATCATC

Exon R1

29001	CTCCCCAAGA	GCTTCATCTC	TCTCTCTCTT	CCCCCTGCCC	TAGCCGGGGT
29051	<u>GGTCAGCGAG</u>	GAGCCATTCA	CACTGAACTT	CACCATCAAC	AACCTGCGCT
29101	<u>ACATGGCGGA</u>	CATGGGCCAA	CCCGGCTCCC	TCAAGTTCAA	CATCACAGAC
29151	<u>AACGTCATGC</u>	AGCACCTGGT	GAGAGGCCTG	CCTCCCGCTG	CAGCCCTGCC
29201	ATGCCCATCC	TAGGGCTGTT	GCCTGCCTGC	CTCTGACCAA	CCCAAGCTCC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)						
Exon R2						
29251	CTTCTCCCTC	TGCAGCTCAG	TCCTTTGTTC	CAGAGGAGCA	GCCTGGGTGC	
29301	ACGGTACACA	GGCTGCAGGG	TCATCGCACT	AAGGTGAGAA	ACTCCCCCAC	
29351	CCACAGCGCA	CCACCAAGAA	CTTAGAGTTC	TGACTGGGAG	GTCCCTCTTG	
29401	GGTTGGGGTG	GGCTACATAT	TTTTTTAAAT	CTTTTATCT	TTCCTTTTTT	
29451	TTTTTTTGAG	ATGAAGTTTC	GCTCTCGTTG	CCCAGGCTAG	AGTGCAATGG	
29501	CACGATCTTG	GCTCACTGCA	ACCTCTGCCT	CCCGGGTTCA	AGTGATTATC	
29551	CTGCCTCAGC	CTCCCCAGTA	GCTGGGATTA	CAGGCAGGCA	CCACCATGCC	
29601	TGGCTAATTG	TTTTGTATTT	TTAGTAGAGA	TGGGGTGTCT	CCATGTTGAT	
29651	CAGGCTGGTC	TTGAACTCCT	GACTTCAGGT	GATCCACCCT	CCTCAGCCTC	
29701	CCAAAGTGCT	GGGATTACAG	GCGTGAGCCA	CCATATCTGG	CCCCATTCTT	
29751	TTTTTTTAAA	TGAATTTAAG	GAGTGCAAAT	GCAGTTTTTG	TTACATGCAT	
29801	ATATTCCATA	GTGAAGTCTG	CAGACAGTAG	ACTTCCAGAC	AGTAGCTTCT	
29851	GGTGTATCAC	CCGAATAGTG	TACATTGTAC	TTATTAAGTG	AGGTTCCCCA	
29901	CCCTTCTCCC	ACTCTCCAC	CTTCTGAGT	ATCCAGTGTC	TATTATTCCA	
29951	CACTCCAGGT	CCATGCTCTC	ACGTATAAGT	GAGAACGTAT	GGTATTCCAC	
30001	CATGAGCTAA	TGGACATGGA	GTCCATTGGC	TCCCACTTAT	AAGTGAGAGC	
30051	ATGCGGTATT	TGACTATTTT	TGAGTTTCAC	TTAAGATAAT	GGACTCCCAT	
30101	TCCATCCATG	TTGCTGCAAA	ATACATGATT	TCACTCTTTT	TATGGCTGAA	
30151	TAGTATTTTCG	TGGTATATAT	ATATACCACA	TTTTCTTTAT	CCAGTCTTCT	

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
30201	ACTGATGGAC	ACTTAGGTTG	GGTCCATACC	TTTGCTGTTG	AAATAGTGCT
30251	GCAATAAACA	TACACGTGCA	GGTGTCTTTC	TTATATAAAT	GATTTCTTTT
30301	TTTCTTTCCT	TTTTTTTGAT	ATAACGAATT	TCTTTTATTT	GGGTAAATC
30351	CCCCAATAGT	GGGATTGNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
30401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
30451	TGACCTGTCC	GTATTGATAT	ATAAAATGCT	GCATTTAAAG	TGTACAACTT
30501	GATATTTTGG	TATACATTGT	TAAATCATGG	CCACATTTCA	GCTAATTAAT
30551	ATATCTATTA	TCTCTACATA	GTTATCATGT	TTGTACCCTT	TGACCAGCAT
30601	CACCCCATTT	GCTCCTCCTC	CCAGCCCCTG	GCAACCACCA	TCCTACTCTC
30651	TGCTTCTATG	AGTCTGACAA	TTTtagattc	CACCTATAAG	TTAGATTATG
30701	CGGTATTTGT	CTTCTGTGTC	CTGGCTTATT	TCACTTAGCC	TAATGTCCTC
30751	CAGCTCCATC	TATGTTATCC	CAAGTGGCAG	GATTTTCATC	TTTCTTATAT
30801	ATTTcattgt	ATATGTGTAT	GCCACATTTT	CTTTACCCAT	TCATCCATTG
30851	AAGGTCATTT	AGCTTGTTTC	CATATCTTGG	CTATTTTGAA	TAGTGCTGCA
30901	ATGAACATAG	GAGTGCAGAT	ATCTCTTTAA	GATACTGGTT	TCATTTCTTT
30951	CTTTCTTCTC	TTTTTTTTTT	TTCTGAGACA	GAGTCTGACT	CTGTCGCTCA
31001	AGCTGGAGTA	CAGTGGTGCA	ATCTTGCTC	ACTGCAAAC	CTGCCTCCTG
31051	AGTTCAAGCG	ATTCTCGTGC	CTCAACCTCC	CAGGGAGTTT	TGCTCTTGCT
31101	GCCCAGGCTG	AAGTGCAGTG	GTGCAATCTT	CACTCACCAC	AACCTGTGCC
31151	TCCCGGGTTC	AAGCGATTCT	CGTGCCTCAG	CCTCCCAGGT	AGCAAGGATT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
31201	ACAGGCGCCC	AACACCACAC	CAGGCTAAAT	TTTTTTGCAT	TTT TAGTAGA
31251	GACGGGGTTT	TGCCATGTTG	GCCAGGCTGG	TCTCAAATTC	CTGGCCTCAA
31301	GTGATCCACC	TGCCTCAGCC	TCCTGAAGTG	CTGGGATTTT	ACAGGCATGA
31351	ACCACCACAC	ATGGCCTCAT	TTCTTTTAGA	TATATATGGG	TTGAGCTATT
31401	CTCAGAGGGT	CCTTTTCTGC	ATCTATTTAA	GATCACATTT	TTTTTATATT
31451	GTGGCAAAA	TACATGTAAC	ATAAAATCTG	CCATTTTAAC	CATTTTAA
31501	TGTACAATTC	AGTGACATTG	ATTATATTCA	CAATGTCATA	CAGCCATCAC
31551	CACTATTTAT	TTCTAATACT	TTTCCATTGG	GTAGATCCCC	AACAGTGGGA
31601	TTGCTGGGTC	AAATGGTAGT	TCTGATTTTT	TTTTTTTGTT	TTTTGAGAAA
31651	TCTCCATACT	GTTTTTCATT	TGAGGTTGTA	CTAATTTACA	TTCCCACCAA
31701	CAGTGTATAA	GAGTTTCCTA	GGCCGGGCAT	GGTGGCTTAT	GCCTGTAATC
31751	CCAGCACTTT	GCGAGGCCCA	GGTGGGTGGA	TCATGAGGTC	AGGAGATCGA
31801	GACCACCCTG	GCTAACATGG	TGAAACCCCG	TCTCTACTAA	AAATGCAAAA
31851	AATTAGCCGG	GCGTGGTGGC	GGGTGCCTGT	AGTCCCAGCT	ACTGGAGAGG
31901	CTGAGGCAGG	AGAATGGCAT	GAACCCTGAA	GGCGGGGCTT	GCAGTGAGCT
31951	GAGATCGCAC	CACTGCACAC	TTCAACCTAG	GCGACAGAGC	GAGACTCCAT
32001	CTCAAAAAA	AAAAAAAAA	AAAAGGTTTC	CTTTCAGTGC	ATCCTTGCCA
32051	ACTTGAGTTT	TCTGGGTTGG	TTTGCACTCT	CATGGTATTT	ACTAGATACT
32101	TCTCCATTTA	TATTTTTACT	CAACCCATGC	CCATAACACC	ACTCCTCTAC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
32151	CATTCCCACC	AACCATGTAT	AAGAGTTCCT	TTTCTTGCAT	CCTTGCCAAC
32201	TTGACTTCTT	TGGGTCAGTT	TGCACTCTCT	TGGTATTTAC	TATTTACTTC
32251	TCCATTTATA	TTTTTAGTCA	ACTGATGCCC	ATGGCACCGC	TCCTCTGAGG
32301	CAGGTGCTGG	GTACTAGAGT	GATAAGACAG	ATGCTGTCCC	TGCCCTCACC
32351	CAGTGGAGAA	GAACAGATGC	TAAACAGGAA	CATAAATATC	TAAGTAAAAT
32401	GGCTTCAAAT	GGAGTAAAGT	GATATGAAAC	ATAAATAAAT	AGCAAGTGAT
32451	GGGTAGAGCA	ACTTTACCCA	GGATGAATCT	TGGGCTGTGT	CCCAAATGGC
32501	CATGAAAAC	GTTCCAGGCA	GGGAGAACAG	CATGAGAAAA	GGTCTTGAGG
32551	TGCAAATGAG	CTTGGCATGT	TCTATGAACA	GCAAAGAGGC	CAGTGTGGCT
32601	GGAGCAGAGA	GAGAGCAAGA	AGAAAAGAGA	GAAAGGATGA	GACTCAAGAC
32651	ATCAGCAAGT	TTGAAGGGCC	TTGGAGGACT	TGGATTTTTT	TTTTTAAGAC
32701	AGCTTTGTTC	TTGTTGCCCA	GGCATGATCT	CGGCTCACCA	CAACCTCCGC
32751	CTCCTGGGTT	CAAACGATTC	CTCTGCCTCA	GCCTCCCAG	TAGCTGGGGG
32801	TAACAGGCAT	GTGCCCACCA	CACCTGGCTA	ATTTTGTATT	TTTAGTAGAA
32851	ATGGGGCTTC	TCCATGGTTG	GTCAGGCTGG	TCTCGAACTC	CCGACCTCAG
32901	GTGATCCGAC	CGCCTCGGCC	TCCCAAAGTG	CTGGGATTAT	AGGTGTGAGC
32951	CACTGCACCT	GGCTTGGATT	TTTTTTGTTC	TATATTGTGG	TAACATACAC
33001	ATCACATTAA	ATTGATCATT	TTAGCTATAT	TTCCCGTTCA	GTGGCATCAA
33051	GCACATTCAC	ATTATTGTGC	AACCATCACC	ACTATCATCC	ATCTCCAGAA
33101	CTTTCTCATC	TTCCCAAAC	GAAACTCCAT	CCCCATGAAA	CACTCATTCC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
33151	TCATCCCCCT	CCTCAAGCCT	CTGGCACCCA	CCATTCTACT	TTCTGTCTCT
33201	GTGAATCTGA	TGATTCTGAG	GACCTCCTAT	GAATGGAGGA	ATCATATGGT
33251	ATATGTCCTG	GTTTATACTG	TATGGCTGGC	TTATTTACAC	AAGCATAATG
33301	TCCTCAAAGT	TCATCCATGT	TGTAGCATGT	GTCAGAATTC	CCTTCCTTTT
33351	CCACTTGTAT	GTAAATGCTG	TATTGTGTTT	CTCCATTCAT	TAGGACTTTG
33401	ATTTTTGCAG	GGAGTTGTCA	AGGGGTGCTG	GGTTCGTTGG	CTTCAATATA
33451	ATAAGAGTAA	GCTAAACTGG	TTCATTTCTT	CCTTCGTGGA	GACCATGTTC
33501	TGGTAGGAAC	AGGAACAAAT	AATTTATGAT	TACATAGAGG	GTGACCAGGG
33551	CAGTGACAGG	GGAAGAGTGG	AGGATTGTGG	GACCCAGAGG	AGGCTCCTGA
33601	CCTTGCCTAG	GAAGATAGGA	GGAGGAAGAG	GAGGAGGAAG	AGGAGGAGGA
33651	AGAGGAGGAG	GAGGAGGAGG	AGGGAGTCCT	CTAAGCTGAG	ACCTGGAGGA
33701	TGACCAGGAA	GTTATCCAGG	TAAGGAGAAA	TGGGGAGAAG	CTTCCAGACA
33751	AAAGTAACAG	CAATTGCAAA	GATCCTGAGA	TGATAGATAA	GGTCAGGTGG
33801	AGAAAGTGCA	AACTGTCAAT	GAGACCAAAA	TATGGACTGT	GAGTTGTGCA
33851	GTGACCACAA	GTGGAGAGGT	GCTAGGTGGC	CTTCATCCCC	CAAAGCTGCA

Exon R3

33901	CCTCTCCCTC	CTCAGGTCTG	TGAAGAACGG	TGCTGAGACA	CGGGTGGACC
33951	TCCTCTGCAC	CTACCTGCAG	CCCCTCAGCG	GCCCAGGTCT	GCCTATCAAG
34001	CAGGTGTTCC	ATGAGCTGAG	CCAGCAGACC	CATGGCATCA	CCCGGCTGGG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
34051	<u>CCCCTACTCT</u>	<u>CTGGACAAAG</u>	<u>ACAGCCTCTA</u>	<u>CCTTAACGGT</u>	GAGCAGCTAT
34101	CAGCCCCATC	TCCCTGCCCC	ACCCCCCAGC	CCCCACTGCA	GTCCAGGAGG
34151	GTGTCTGTTT	GCCGGTTCTC	TAGGGAAAGA	CTTGGGGTTC	AAGTCTTGGC
34201	ATTACCACTG	GCCCTCCCAT	AACCACAATG	CAAGGTTGGA	CTTTGATTAA
34251	TCCCATTTTA	CAGATGAAGA	AACTGAGGCT	TAGACAGGCT	AAGCAATTTA
34301	CCTTGACAGT	GGTGGAACCA	GGATATGAAC	TCCACTTGTC	AGCATTCGGT
34351	GCTATGATCC	ACTCCACATG	TTTAACTCAC	AGAAGAGTCT	TCCTGGTGGG
34401	GGCACTTGGG	GGACAAAAAA	CACATTTCCG	GCTGTGAGCA	GTGGCTCACA
34451	CCTGTAATCC	CAGCACTTTG	GGAGGCCAAG	GCGGGCGGAT	CACAAGGTCA
34501	AGAGATTGAG	ACCACCCTGG	ACAACATAGT	GAAACCCTGT	CTCTACTAAA
34551	AATACAAAAA	TTAGCTGGGT	GTGGTGGCGC	ACGCCTGTAG	TCCCACCTAC
34601	TCGGGAGGCT	GAGGCAGGAG	AATCGCTTGA	ACTCGGGAGG	CAGAGGTTGC
34651	AGTGAGCCAA	GATTGCGCCA	TTGCACTCCA	GTCTGGGTGA	CAAGAGTGAA
34701	ACTCTGTCTC	AAAAAAAAAA	AAAACAATTT	CCCCTCCCTG	CTTCTTCTC
34751	ACCATTGACG	AGGGATGGGC	TTCTCTCCTA	CCTGAGGCCC	CCTATACCAG
34801	GAAGATCTAT	GGGATCTAAT	CTTCAGCGCA	CACTGGGCCT	CAGCATTGGT
34851	CTAGAACTCA	GGATAAGATA	GCATTTAAGA	AGGCATCCCC	TAAATGGGGT
34901	TCTGAGAGGC	AAAGCATGAC	CGTGGAGAAT	TGACAAAATA	GCTCGCCTTT
34951	CATCCCCTCC	ACCGCCAACC	CAAGAACAGT	GCTTATCATC	ATGACCCCAT
35001	GAGGTGGGCA	CCCCATATCA	CTTATATGAG	GTACCTTTAG	GTAGGTACCG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
35051	GGATGTGGAG	AGACATCCTG	GGCTTTCATT	ACTCTTATTT	TAGCAAAGAG
35101	GGAATCTGAG	GCACAGAGAA	GGAAGGGAC	TTGCCCATGC	CCACAGCGAG
35151	TTTTTGGCTA	GTATGGGTCT	TGATGTTCTT	TCTGGGTCCG	TNNNNNNNNN
35201	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN
35251	NNNNNNNNNT	TCCTGCGTGG	GAGATGTGTG	GATTTGATTT	GTATCTGGAA
35301	AGATGATTTT	TTATTGGTGA	CAAAGCAGTT	AAAGTTAATC	TTCACAGTTG
35351	TGCGGAGAGT	GACCACGCGA	GTTAGTCTTA	TCCTTATTTT	TTTGATCATC
35401	CCGCTACACA	AGACAAAGCG	AACCGCACAG	GCAACATCAG	CAGGCCCAT
35451	TGGTGTGTTT	CCCTCTATGG	GTCCATGTGT	TCTCATCATT	AGCTCCCACG
35501	TATAAAGTGA	GAAGATGGCA	GTATTGGTTT	TCTGTTCTCG	CATTAGTTTG
35551	GTAAGGATAA	TGACCTCCAG	CTCCAACCAT	GTTCTTGCAA	CGGACATGAT
35601	CTCATTCTTT	TTTATAGCTG	CATAGTATTC	CATGGTGTAT	ATGTTCTCTCA
35651	TGTTCTTTAT	CCAGTCTATC	CTTGATGGGC	ATTTAAGTAG	ATTCCATGTC
35701	TTTGCTATTG	TGAATAGTGC	TTCAGTGAAC	AGGTGTCTTT	ATGATAGAAA
35751	AATTTATATG	CCTTTGGGCA	TATATGCAGT	GATGAGATTG	CTGGGTCAGA
35801	CGGTAGTTCT	GTTTTTAGCT	CTTTGAGGAA	TCATCCTGCT	GCTTTCTACA
35851	GTGGATGAAC	TAATTTACAC	TCCCACCAAC	AGTGTATAAA	CACTCCTTTT
35901	TATCTGCAAC	CTCAGCAGCA	TGGTTTTTATT	TCTCTTTATG	GCTGAATAGT
35951	GTTCCATTGT	GCATATATAC	CACACTTTCT	TTATGGATTG	ATCTGCTGAT

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
36001	GGACATATAG	GTTGATTCCA	CATCTCTGCT	ATTGTGAATA	GTGCTGTGAT
36051	AAACACACAG	GTGCGGGTTG	GGTCTTGATG	ATCTCAGTTA	ACATCCAGTC
36101	CCTTCAACTT	GGCTATTGCA	GGGAGCTGTT	CCCCCTTGTA	AACTGCACAG
36151	CTTATGTGCT	TCATTTTGTT	CCTTCATTTA	GATTTACCAA	GCAGCTACTA
36201	TTAACCAGGC	CACAATGTGC	CTCGCCCCCA	GGAACAGAGA	TAGGTTACAT
36251	GTGCATCCTG	TCCTAATGTA	ATCTCCAGGG	GGGCGGAGAC	TGTTTTGTTC
36301	TACCCTATAT	TCCCCAAATG	TAAAGGGAGC	CTTGACACATA	CTAAGCCCTT
36351	AATAAACATT	CATTGGGTGG	AGGAATAGAT	TGGAGGAGGC	CTGGAAGGGG
36401	AGGCGGGGGT	TATGGATGGA	TAGGAGGATA	GACTTGTGAA	CACAAAGGTA
36451	GTGAGAGCCT	CTCATTGGAG	GCATGCTGGA	GACGTGAGTA	GGGAAGGGTC
36501	AGTGCTAATT	GAAATATCAG	GAAATTCTTT	CTAGTGGTGA	ACACATTTAA
36551	GTCAAATATT	AGATGATACA	TAAATGTATC	CATAATCTCT	AGATACACAA
36601	AGGGAAAGGC	ATCCAGGCAG	GGGCCCCATA	TGGACAAAGG	CATGGAGTAT
36651	CTGGGACGGT	TCCACCACCT	CCTCTTACGT	GTGACTTCTT	TGTTTCAAGG

Exon R4

36701	<u>TTACAATGAA</u>	<u>CCTGGTCTAG</u>	<u>ATGAGCCTCC</u>	<u>TACAAGTACG</u>	TGTCTTTGAA
36751	TCTAGTGCCC	ATTTCAATCT	CCATGGGTCT	TGGTTCAAGC	TTTCTCCTC
36801	ATTCATGAAG	GAAGGTTGCC	CCAAATTCGG	GCTGGTCCCC	TAGGTGGTGA
36851	GGGGCATTGT	CTCAGTGGGA	GGAAGAATGC	TGAGTCCTTG	GCCCTGTTTT
36901	TAGACCTGCA	GCCATAGTCT	TGGCTTTGTG	AATTTTCCAT	GTCCCTCTGG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
36951	GTTGGAGGAA	GAAGTTTGAA	CAAGCATTCC	CTACACGGGA	TAGAGGTTGA
37001	GGTCAGATGA	TGACCTCTGT	TAGTCTGTAC	CCTCCTTGAT	AAGAAAATCT
37051	CCTCCAAGTG	CCCCAGCAGA	GGCTTCATGG	TCAAGCTGCA	GACTCTGCTG
37101	GCTACTGGTT	TTGGCTAAAT	TTGCCATTG	CCTCATCCAG	TGATCCACTC
37151	GTCTATCTTT	CCAGCCATCC	ATTTTCTAT	CCTTCCAGTC	ATCTCTCAGA
37201	CACCACCTGT	CCTTCCATCC	ATCCATCCGT	CCATCCATTT	ACCCATCCAT
37251	CCATCCACCC	CATTTTCCTG	ACCATTTACC	TCCTCGTCCT	TCCTTCCATC
37301	TGTCCTTTTA	TCCATCTATT	CATCCATCAC	CCATCCTCCT	GCCCATTCAC
37351	CTGCTTGTCC	CTCCTTCTT	CTGTCCTTCT	ATACATCCAT	CCATCCATCC
37401	ATCCATCCAT	CCACCCATCC	ACTCATCCAC	CACCCACCCA	TCCTTCTGCC
37451	CACTCACTCG	CTAGCCCCTC	CTTCCTTCTG	TCCTTCCATC	CATCCATCCA
37501	CCCATCTTCC	TGCCCATTCA	CCTGCTTGTC	CTTCCTTCTA	TCTGTCTTTT
37551	ATCCATCTCT	CCATCCATTC	TCACCATCCA	TCCATCCATC	CTTCTCCCTA
37601	TTCACTGGTT	TGTCTTTCCT	TCTGTCCTTC	CAACCATCCA	CCCATCTCTC
37651	CATTCATTCT	CCTCTTCATT	CACCATGTTT	CCTTATTTCT	GTCTCTTCCA
37701	TCCATCCATC	TATCCAGACA	GACATCTCCT	CCCCCATTC	TCCTCCCCAT
37751	TCACTCAATT	GTCCTTCCTT	CCATCTGTCC	TTTTATCCAT	CCATCCACCC
37801	ATCCATCCAT	CCATCTATCC	TTCTCCCCAT	TCACCTGTTT	GTCCTTCTTT
37851	CTGTCCTTCC	AACCATCCAT	CCATCCATCA	TCCATCCATC	TATCCTTTTC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
37901	CCCATTACACC	TGTTTTGTCC	TTCCTTCTGT	CCTTCCAACA	TCCCTCCATC
37951	TCTCCATCCA	TCCTCCTGCC	TATTCATCTG	CTTGTCTTTC	CTTCCTTCTG
38001	TCCTTCCATC	CATTCATCCA	TCTGCCCATC	CACCCACTCA	TCCTCTTGCC
38051	CATTACCTG	CTTGTCTTTC	CTTCCACCTG	TCCTTTTATC	CATCCATCCA
38101	TCCATCCATC	TTGCTCACTC	CTCCACTCAC	ACAATCACTC	CTTCCCTCAG
38151	TCTCATTTAT	GGCCACCTG	TGAATGGTTG	TCCTGGCTTG	GACCACTGAT
38201	GAAGCCCAGG	GGAGCTTCTC	CCACTAGTGG	TGGGCTTTTG	TCCTCTCTGA

Exon R5

38251	TGGACTGTTC	CTTCCACAGC	<u>TCCAAGCCA</u>	<u>GCCACCACAT</u>	TCCTGCCTCC
38301	<u>TCTGTCAGAA</u>	<u>GCCACAACAG</u>	GTATTTGGGG	CCATTTTTC	TCCTCGAAGA
38351	TTAGAATAGC	ATTTCAATCA	GACACCTGCC	CTCGTGGAGT	CCCAGATTTT
38401	ATGAAATAAA	TAGACCATCA	TAATGTCAGA	TGTTTTGGGG	TGAGATACCT
38451	GGCATAGTTG	GGAAGGAGGA	GGGCTTTCTG	GAGAAAGTTT	CACCTGAACT
38501	GAGTCTTTAA	GGATGACTAA	GAGTGATTCA	GGCAAATAGG	GCATGAATAG
38551	TATAACTGAA	AGAGGGGAAT	CTGTGAGCAA	AGCCTCAGTG	GCCAGAAACA
38601	GCATAGAGTA	TAGGGAGAAG	TGAGAGAAAT	TTGGTTTGCA	TGAAACATAA
38651	AGCTTAACCC	AGAGTGGATG	GATAAGTGAG	ACTGAAAGGT	CAGCAGGAGC
38701	CAGATTGGGA	AGGGCCTTGA	ATGCCAAGTC	AAGAAATTTG	AACTTAACAC
38751	TGAAGGCCAT	AGGGAGCTGT	GGATGGTACT	AGAGCAGGGG	CAGCCATAGT
38801	GAGATTGTCA	TTTCAGAAAG	ATTCTTCTTG	TGTTCAGTAT	AGAGAATGTC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)	
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38851 CTTTAGACAG GGCATCCAGT GAGTCTGCCA GGTGCTAATC AGGGTGAGAG
 38901 AAAATAAGAC CTGAACCTGGG ATAGGGGGAG GAGAGAGAGG ATATATGTGA
 38951 TGAATATTCA GTAAAGAGAA TTGGTGTTAC TTGGAGGGGA GAAGACACAT
 39001 AGCTTCTGAC TTGCGATGGC CACACTCAGT TTAATAATGA GCGCAGTCTG
 39051 ATCTAGTCTC AGACCAGCCC TCAGTTGCAG ACGTCTCTCC TCCCCTCCTG

Exon R1

39101 CAGCATGGGG TACCACCTGA AGACCCTCAC ACTCAACTTC ACCATCTCCA
 39151 ATCTCCAGTA TTCACCAGAT ATGGGCAAGG GCTCAGCTAC ATTCAACTCC
 39201 ACCGAGGGGG TCCTTCAGCA CCTGGTGAGA CCCTGGTCCC AGCAGCTCCT
 39251 GGTGGGATAA ATCCTACCCC CAACCTCTGT TCCTCGGCTT ACCCTCTTCC

Exon R2

39301 TCCTTCCTCT CAAGCTCAGA CCCTTGTTCC AGAAGAGCAG CATGGGCCCC
 39351 TTCTACTTGG GTTGCCAACT GATCTCCCTC AGGTGAGACC ACTTCCTGGC
 39401 CATTTGCCAG TAACAACCAC CCCTTTTGTG ACCACCCCTT CCTCAGCTTT
 39451 CCCCTGCTCC TCCCTCCACT GCTCTTTACC TGCAGAGGTC TCGGGACCTC

Exon R3

39501 TCTAGAGTCC TCAAATGCCT CTCTCCCCAG GCCTGAGAAG GATGGGGCAG
 39551 CCACTGGTGT GGACACCACC TGCACCTACC ACCCTGACCC TGTGGGCCCC
 39601 GGGCTGGACA TACAGCAGCT TTAAGTGGAG CTGAGTCAGC TGACCCATGG
 39651 TGTCACCCAA CTGGGCTTCT ATGTCCTGGA CAGGGATAGC CTCTTCATCA

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
39701	<u>ATGGT</u> GAGTG	TCAGGCTGAA	CTTGGATTTA	CAGTGACTTT	TGGGGAGTTG
39751	GTTTCTTTGT	TTTTGAGATG	GAGTCTCACT	CTATCACCCA	GGCTGGAGTG
39801	CAATGGTGCA	ATCTTGGCTC	TGCAACAGTG	ATTCTCCTGC	CTCAGCCTCC
39851	CAAGTAGCTG	GGATTTACAG	GTGCATGCCA	CCACGCTCAG	CTAATTTTTG
39901	TATTTTTTAGT	AGAGATGGGG	TTTACCATG	TTGCCCAGGC	TGGTCTCGAA
39951	CTCCTGACCT	CAGGTGATCC	ACCTGCCTTG	GCCTCCCAA	GTGCCAGGAT
40001	TACAGGCATG	AGCCACCATG	CCCGGCCAC	CATGACTATT	ATTTGTCCCT
40051	GTTGTATGCC	CTTTCCTCTC	TAAAAAAAT	AGCCCAAGGC	CTGGCTGGGG
40101	GACACCCTTC	CCCAAACCAC	CAAGGGGAGG	GTCTTCCCA	TTATTTTGAG
40151	TAAATAGCAT	GAAATTCTTT	GACCAAATTA	ATGTCATAAA	TTGTTTGTCT
40201	CTTCTCCTT	CACTTTTGTT	TCCAACCTGG	TTGCGGTATA	ACTATCAAAT
40251	ACAATTGTAT	GTATTTAAGA	TGTATAATGC	AGTGATTTAA	TATATGTGTA
40301	GCTTATGAAA	TGATTACCAT	GATCAAATTA	GTTAACACTG	CTTTCATGTC
40351	ACATAGTTAC	CGTGTGTCTG	TGTGCGTCTG	TTGAGTTAG	AGAGAAAGAG
40401	AACATTTAAG	GTCTACCCTC	ATAGAAAATT	TCAGGTTTAC	AATACAGTAT
40451	TATTAECTAT	AATCATCAAG	CTTTATACTC	GATCCCCAGA	ACTTATTCAT
40501	CTTGTAECTA	AAAGTTTGTA	TTTTGTGACC	AACATCTCCC	CATTTTCTCT
40551	ATCACCACCC	CCATGCCCCC	AGCCCCTGAT	AACCATCATG	CTACTCTCTG
40601	CTTCTGTAAG	TTTGACTTCT	GATCCACAT	ATAAGTGAGA	TCATGCAGTA
40651	TTTGTTTCTC	TCTATCTGGT	ATATTTCACT	TAGCATAATG	AACCCCCCCC

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
40701	AGGTACATCC	ATAATGAATT	TCAATTCAAA	ACCCAAGTGG	CTGAGTCGTG
40751	GCATCCTTTG	GGACAGGATA	GCAGGTCCCT	TCTATATAAG	GATCCTCTGT
40801	GTCAGTGGTT	ATTACCAGGG	GACAATTCTG	CACTTCTGCC	CCACCCCACC
40851	CCCCAACTGG	GAGACTCTAG	GCAATATCCG	AAATCATTTT	TGGGTATCAC
40901	AACTCAGGGA	GGGAAGGAGG	GTGCAACTGG	CACCTAGTGG	GTCGGTAGCC
40951	CATTTTCCAG	TGCACAGGAG	ACAACCACCC	CAGGGAATGA	TCCAGCCCCA
41001	AATGCCAATA	ATTTCAGGG	TGAGAAATCC	TGTTGTACAT	GGTCTCAAAG
41051	TTCTTAGGTG	GGCACAAGGC	TGACATTTAT	CACACTTTAC	TGTAATTACT
41101	TGTTAAATTT	ATCTGATTCC	CCCTTACCCT	GTGAACTCAA	CAAATTTACG
41151	GTCTATTATG	AGTGCCACTG	TACCCTCGGT	TCGCAGTACA	TCAGCACATC
41201	ATAGTATGGA	AAGAATCATT	GAATGAGTGA	GCAAATTAAA	GATTTGTGTC
41251	TCTGCTGTAA	CTCACATTCA	TTAATTCATT	CATTCAGCAA	ACATATATGG
41301	GTGGCTGTTC	TGCCCCAAGC	CTTGTAAGTGG	GTCTGGAGAT	AGAAGACACA
41351	TTTTTCTGTC	TCTGAAAAAC	TCATACTCAA	GTTAACAACA	AATTACGGGC
41401	ACAACAAAGA	CCCCACTGCT	GTTATTAACA	GGGTACTATG	GGAGCTGAGA
41451	GGAGGAGTAA	ATTAAGGAGG	GCTTCCTGGA	GGAGGGTGTT	ATATACCCGG
41501	CCCTGTGCCG	GGACACATAA	TGATAAGACA	GACTTGGGCC	TCTGCTGTCC
41551	TGGAGCTCCC	TCTCACTGGG	CTCTTGAAGC	GTGAGCAGGA	GTTTTGCAGG
41601	AAATGAAAAG	GATGCATTCC	TAGAAGTGGG	AACTGCATAG	CACATGCAGG

Table 2 (continued)

Genomic Repeats (SEQ ID NO: 2)					
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41651 AAAGCTCAGC TCAGAAGAAT CTGTGTAATA TTCCATTTTT CCCTCTCTTT
 41701 GGGGCAACTT TCTGTCTAAG AGCTCCTGCA ATGCCCAGCG TGTGGACCTG
 41751 AAATTGATTC TGACAGTAGG CAGGGGACTG CTGGGCAACT TTGGCTCTGC
 41801 ATTTTGTGAT CAACATTTCC CCACCATATG TTGCCTTTTC TTCTTCTCTG

Exon R4

41851 TGGCTCCAGG CTATGCACCC CAGAATTAT CAATCCGGGG CGAGTACCAG
 41901 ATAAATTTCC ACATTGTCAA CTGGAACCTC AGTAATCCAG ACCCCACATC
 41951 CTCAGAGTAC ATCACCTGTC TGAGGGACAT CCAGGACAAG GTGGGGCATC
 42001 TCTCACCCCT CCCGTCTTCT CTGTCCTGTG TGCTTCTCTC CCTCTTCTAC
 42051 CTGATTTCTC TGTTAAGTGA TCACTTTAAA TGCTTCACTT CACTATGTAT
 42101 TCTGGGTTCT CTCTCAGTTT CAAAAGTAC TCTCTTGACT ACCATTCCCA
 42151 TTTCACAGAT GGGCAAACCTG AGGCTCAGAA AGGGGCGTGG TGTGCCTAGG
 42201 GTCATACAGT GCTTTAGGAA CAGAGTTAGG ATTTGAACTC TGGTCCCCTT
 42251 TGCTCCAAGT CCTGTGTTTT TTTCCACTGG CATCAGCGGC CCCTCCACCC
 42301 CCAAGAGGCC TCCATCTCAC CCACTCTCCC TACCCATCTT TCTAGGTC

Table 3

Genomic Carboxy Terminal
(SEQ ID NO: 3)

Exon C1

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1  ACCCACTCT ACAAAGGCAG TCAACTACAT GACACATTCC GCTTCTGCCT
51  GGTCACCAAC TTGACGTAAG TTCTGAAGGT CATAAGCAGT GACCAAGCTT
101 GTGGCTGTGT CTCTGAGCAC CCTTGAGCTA GACGTCCCCA GTGGGGTACC
151 CATTCTCCCC TACATCCCTG TCTAGCTAAT CCTACCATCT CCTCCCATAA
201 ATCCTCAAGG TAGGGAGTGA GGATTAACCT CATGGGGCCA CCAACTCCCCA
251 GCATACACCT TCTTTTTTTT CTGGACACTT GGGAAAATAT AACTTTTTTGA
301 TGTAGAACTC AAAATATTAG CCCAATAATA ATATTTAACA TCAACCAGCC
351 TCCTCTCATT TAATTCTCAC AACAGAATCT ATGAGTTGAG TGCAAAAATC
401 ATCCCTATTG TGCAGATGGG AAAACTGAGG GTCAGAAAAG TGAACCTCCC
451 AAGAACTGTC AAAGTTGGGA TTTGAACCCA GGTCTCTGAT GACTGGATGA
501 AGGAATGAAG ATACCTATAC TTGGGAATGA GGAGGGTCGA CAGGACACGA
551 GGGCTGACTT TGTATATTTT TAAACTTCAA AGATTTTCTG TATTTTCAGCT
601 GGGAATATGG TAGAAGGTTA ATTGGAACAA AAAAATGCAA AGCAATGAAT
651 AAGACCTCAG TATTTGCTAT GCACAACAGG GTGACTGTAG TCCCACAAAT
701 AACTTCACTG TACATTGTTA AAATATAACT AAAGGTGTAT GCTTGGATTG
751 TTTGCAACAC AAAGGATATA TGCTTGAGGG GATGGATACC CCATTTACCC
801 TGATGATTAT TATGCATTAC ATGCTTGTAT CAAAACATCT CATATACCCC
851 ATAAATATAA AAACACCTAC TATGTACCCC AAAAAATTAA AAACAAATAA
1051 AGGCATGGTG GCACACACCT GTAGTCCCAG CCACTCAGGA AGCTGAGGTG
1101 GGAGGATCGC CTGAGCCTAG GAGGCTGTAC TCCAGCCTGG GTGACAGAGC
1151 GAGACTCTAT CTCAAAAAAT AAAATAAAAT AATAAAAAGT AGAAATCAAG
1201 AGGGAAAATG TGGGAGAAAT TGGGATAATT TTAACAATAC CTTCCACCAG
1251 AGTGATGATG AAGAATGCAT AAGTCACTTC TTAGTGGTCT TGATCTATAA
1301 AAAGTGTTCA ATAAATATCG ATTATTGTTA CTGTTATTGC TTCTAGACGT

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Table 3 (continued)

Genomic Carboxy Terminal
(SEQ ID NO: 3)

1351 AATTCCTGGA AGCATTTTTT TTTTTTTTTT TTTTGAGATG GAGTCATGCT
 1401 CTGTTGCTCA GGCTGGAGTG CAGTGGTATG ATCTCGGCTC ACTACAACTG
 1451 CCTCCTGGGT TCAAGCAATT CTCCTGCCTC AGCCCCCAT GTAGCAGGGA
 1501 CTACAGGCAT GCGCCACCAC ACCCGGTGAA GTTTTGTATT TTTATTAGAG
 1551 ACAGGGTTTT GCCATGTTGG TCAGGCTGGT CTCGAACTCC TGACCTCAGG
 1601 CAATTTGCCT GCCTCGGCCT CCCAAAGTGC TGAGATTACA GGCTTGGGCC
 1651 ACTGCATCCA GCCGAAGGCC TCCCATTTTG ATCAGAACCC TTCTCTAGAC
 1701 TGAGGGTGGG TGCCTCTAGA TCTTTTGCTC TTAAAGACA GCAACCGATG
 1751 ACCCTGCTGA TGCTGAGTAC TGGCTGAATT CCTGTGGTCT CTGTCCCTAG

Exon C2

1801 GATGGACTCC GTGTGGTCA CTGTCAAGGC ATTGTTCTCC TCCAATTGG
 1851 ACCCAGCCT GGTGGAGCAA GTCTTTCTAG ATAAGACCCT GAATGCCTCA
 1901 TTCCATTGGC TGGGCTCCAC CTACCAGTTG GTGGACATCC ATGTGACAGG
 1951 TACAAGGTGG GGTGGCTGGT TTCCTAACTG GAAGAGGTGG GGTTATGAGG
 2001 AAAGATGGGG CTTCTCGGTA CCAGTGGAAAT TGGTGGAGGC TCTAGAGAGG
 2051 GAAAGGGAGG CTTTCTGGAG ACCCATGTAG GTGACCTCTG GCAGTAGATC
 2101 ATCCAACGAG GCAGGAACAG AACACCAGCC ATTGCATCTA AGAGAATAGC
 2151 TATTTTTTACA TGTA AAAAGA ATTGTGTTGA ATGAATGAAT CAATAGATCA
 2201 TTTATTTTGA ATCAATTTAT TGATTCATTC ATTTAATTAA TGAATAATAA
 2251 ATGATTCAGT ACATAATTGA TTAATTGATG TAATTGAGAA TTGATTTAAT
 2301 TGATTAATTG ATCAATTAAA ATGATCAATT AAATGAATGA ATCAGTAAAT
 2351 GAATAATTCA TTCATTCAAT AAACAATGGA AGTAGGCCGG GCATGGTGGC
 2401 TCACGCCTGT AATACCAGTA CTTTGGGAGG CCCAGGCAGG CAGATCACGA
 2451 GGTCAGGAGA TTGAGACCAT CCTGGCTAAC ACGGTGAAAC CCTGTCTCTA

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
2501	CTAAAAATAC	AAAAAAAATT	AGCCAGGCAT	GGTGGTGGCC	ACCTGTAGTC
2551	GCAGCTACTC	GGGAGGCTGA	GGCAGGAGAA	TGGCGTGAAC	CCGGGAGGCA
2601	GAGCTTGCAG	TGAGCCGAGA	TCGCGCCACT	GCACTCCAGC	CTGGGCGACA
2651	GATGGAGACT	CTGTCTCAAA	AATAAATAAA	TAAATAAAAA	TAAAAAATAA
2701	ATAACAATG	GAAGTAAACA	CGTACTGATA	ACACAGTGTG	ATCATTGCTA
2751	TGATAAGGGA	ATTTCAGGGG	CCTGTGGGAG	CCCCAAGGAG	GAACACACAA
2801	CCTTGTCTTG	GAAAGTTTTA	TGTAGGAAGG	GGTGAAGAAG	CTGAGATCTG
2851	ACAGAGAATG	GGACCTAGCC	AGGGGTAATA	GATGGAGAAT	TGTGCTCCAT
2901	GCATCTATAA	CCTAGAAGAT	AGAAAGAATA	TGGCATCTGG	CCGGGTGCGG
2951	TGGCTCACGC	CTGTAGTCCC	AGCACTTTCA	GAGGCTGAGA	TGGGTGGATC
3001	ACCTGAGGTC	AGGAGTTCAA	GACCAGCCTG	ACCAATATGA	TGAAACCCCA
3051	TCTCTGCTAA	AAATACAAA	ATTAGCCAGG	CATGGTGGTG	CGTGCCTGTA
3101	ATCCCAGCCA	CTTGGGAGGC	TGAGAGAGGA	GAAGTGTGTTG	AACTCGGGAG
3151	GCGGAGGTTG	CAGTGAGCCG	AGATTGTGCC	ATTGCACTCA	AGCCTGGGCA
3201	AAAAGAGCAA	AACTGCATTT	CAAAAAAAAA	AAAAGTGGCA	TTTTGGGGCA
3251	AGTTTAAGAA	GATTGGTGTA	GCTGGAGCAT	CCACTTTGAT	ACTGGAGAGG
3301	TGACAGTTGA	AGCCAAAGAT	GTGGGCAGAG	ACTTTGTTGG	GCACTGGAAT

Table 3 (continued)

Genomic Carboxy Terminal
(SEQ ID NO: 3)

3351 GGCTTGGGGA GGAACATGAC AACTCATGA GTTCTGCTTT AGAAAGAAAA
 3401 TGAAATGAAT TCTGCTCATC CTCTGGGTGC TGTGTGCAGA ATGGAGGGTG
 3451 GGGGGAGAGA AGAGCAAAGG CAAGAAGACC CTTTAGGAAC AATGATCATT
 3501 AGTTAGAAGA CTCTGGGTTT CTCAGCACCT GCAATTGCTG ACTACACCCC
 3551 CAGAGAAACC CAGTCTCTTT TCCCCATGT TGTAGAGAAT TCTTACAATG
 3601 CTTGGTAGAA AGAGAATTGA ACAGGTAGAT GGGTGGATGG ATACAAGCTG
 3651 GACAGATGGA TGGAGGAAGA TCCTCCATCC AATATAGAGC TGTTACCTAA
 3701 AACCTCCAT CCCACCTTTA AAATCCTAGC TCAGCCAGGC GCGGTGGCTC
 3751 ACACCTGTAA TCCCAGCACT TTGGGAGGCC AAGGCGGGTG GATCACTTGA
 3801 GGTGCGGGGT TCGAGACCAG TCTGACCAAC ATGGTGAAAC CCCCTTCTCC
 3851 ACTAAAAATA CAAAAAATA AAAAAGTTAG CCAGGCAGGG TGGCGCATGC
 3901 CTGTAATCCC GCTACTCGGG AGGCTGAGGC AGGAGAATGG CTTGCACCCA
 3951 GGAGGTGGAG GTTGTGGTGA GCCAAGATCA CGCCATTACA CTCCAGCCTG
 4001 GGCAAAGAGA GTGAACTGT CTCAAAAAAC AAAACAAATG ACCCCCCTGC
 4051 CAAAAAATA AAAAAAATA AAGAAAAGAA AAAAAGAAAA GCCTAGCTCA
 4101 GCTCACACTG TCAGGAATAA GTAAGCTAGC TGGAATCATC TCTTTCTTAA

Exon C3

4151 AACCTGCCT TGATAGTGA TTTTACATA CTTTTTTTTT AATTCTAGAA
 4201 ATGGAGTCAT CAGTTTATCA ACCAACAAGC AGCTCCAGCA CCCAGCACTT
 4251 CTACCTGAAT TTCACCATCA CCAACCTACC ATATCCCAG GACAAAGCCC
 4301 AGCCAGGCAC CACCAATTAC CAGAGGAACA AAAGGAATAT TGAGGATGCG
 4351 GTGAGAAGGG GGTGGTATGT CCACTCTGTT GCCATGCAGA AACTGACTTA
 4401 TGCATACTGG GTAGCCACAG GGTGACTTTT TATAACAATC CACAAAGACA

Table 3 (continued)

Genomic Carboxy Terminal
(SEQ ID NO: 3)

4451 GGTTCCTTATT CCCATTTAAT ACACAAGCAC AGAGAGGTTT AGTAGCTGAC
 4501 CCAAGGTCAC ACAGCTAAGT CATACCCTAG AAGAGCATGT CCTTTGATAT
 4551 ACATACCTGG GCAAGTGGTT GTCATGACAA GAAGCAAAAT AGACGGAGAA
 4601 GTGTGCTCAG TGGCTGAAAA TTCTCTGATG CTAAGGGGGC CAGGATTCTG

Exon C4

4651 ACCTAAGAAA CATCGCCCTG TCTTTCAGCT CAACCAACTC TTCCGAAACA
 4701 GCAGCATCAA GAGTTATTTT TCTGACTGTC AAGTTTCAAC ATTCAGGTAA
 4751 GTTCTAACTC AGGACCTAAT GACTCTAGGA ACTTCTGCTG TCCTTTAAAT
 4801 AGAAGTGTCC CCAAGCCATA GCTTTGATGG AAGAGAGCCC TAGAAATAGA
 4851 GAGCTGTTAA CTAAAACTA GCTTTTTCCT AAAGCTGGAG CCCAACTGGC
 4901 TTCAACACTC AAGAGAGCTG GTGTAAATCT CAGCAGACAT AAAGGTACCT
 4951 GGTGCTGAGG CCATGGAGTC TAGAGTGTAG AATCTACTAC ATTAAGACAT
 5001 CAGCTACTGA AATCAGGACC CATGGAAGAC GGGGGAAGGA GGGGACTAAA
 5051 ACCAGATTAC TTAGAATCTA GCAGCCTAAC TGTGCTTTTC AATGAGAGGT
 5101 ATCATTTCCA ATGGTGGGGG GTACCAATGA TTTTTTTTTT TTGACAACTG
 5151 CCTTGAGAAC AGGCTTTCCT CACTAAACAA ATTCTGAATC AGAACAAATA
 5201 AAGATAAGCC CTGAGAATAG GGCTTTTTTCA AGGAGCTGCC AAACAGATCA
 5251 AATAGTGACT ATGTTCTGCA GATTGATGTC TGGAGAACTC TACAGCTATT
 5301 TTGACTGCTA GGCAGCTGGT TTTCACAGAT ATCATGATTC TGAGGCTGCC
 5351 AGTTTTCAAA GTTACCGAGG ATCTTGCTGG ATGCAGTGGC TTGCGACTGT
 5401 AATCCCAGCC CTTTGGGAGG CCAAGGTGGG TAGATCGCTT GAGCTCAGGA
 5451 GTTTGAGACC AGCCTGGGCA ATATGGTGAA AACCCATCTC TACAAAAAAT
 5501 ACAAAAATCA GCTGAGCATA GTGGCATGTG CTGTAGTCCC AGTTACTTAG

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
5551	GAGGCTGAGG	TGGGAGGATG	GCTTGAGCCC	AGGAGGCAGA	GGTTGCAGTG
5601	AGCTGACATT	GTGCCATGCA	CTCTAGCCTG	GGCAACAGAG	CCAAAGCCTG
5651	TCTCAAAAAA	AAAAAAACAA	ATAATAATAA	TAATAAAATA	CTGAGGATCT
5701	TGAAAGAGCA	CTGTGGAAAT	AATGCAAGTT	AAAATGCCAC	AAAGCTTGCT
5751	CTTTTACTG	AGATTTAACA	CTTTCCTTAA	CTAAACACCC	CTCGAATTTT
5801	TGCAAGCCTT	TGGTTCACCT	CTAGACTTCT	GGAAAAATTG	ATTTGGACTA
5851	TTTTGGCCAA	TGTTCTCATT	GATTTTATGG	GTATTCAGAA	GTTGTTACCC
5901	CAACATTCCA	GAAATGTTCT	CCCTGTGGCT	ATTACTTTAT	TTATTTATTT
5951	ATTTATTTAT	TTATTTATTT	ATTTGAGACG	GAGTCTCCCT	CTGTTGCCCA
6001	GGCTGGAGTG	CAGTGGCGCA	ATCTCAGCTC	ACTGCAACCT	CCGCTTCCCA
6051	GGTTCAAGCG	ATTCTCCTGC	CTCAGCCTCC	CAAGTAGCTG	GGATTATGGA
6101	TGTGCACCAC	CACACCGGCT	AATTTTTGTG	TTTTTAGTAG	AGATGGGGTT
6151	TCACTGTGTT	GGCCAGGCTG	GTCTCGAACT	CCTGATCTCA	AGTGATCCAC
6201	CCGCCTTGGC	CTCCCAAAGT	GCTGGGATAA	TAGGCATGAG	CCACTGTGCC
6251	TGACCTCCCT	GTGGCTATTT	TTAAATGAAT	TAAGTGGAAT	AAAATTAGAA
6301	ATTCAGTTCT	TCTCCCACGC	TAGCTGCATT	TTAAGCATTT	AATAACAACA
6351	TGAAGCTACT	AATGGCTGCA	TTGTGTAGTG	CAGATGTAGA	ATTTTTTTTT
6401	TGTTTTTTGT	TTTGTTTTTG	AGATGGAGTC	TCGCTCTGTC	ACCAGGCTAG
6451	AGTGCAGTGG	CGTGATCTCG	TCTCACTGCA	ATCTCTACTC	CCCATTCAA
6501	GTGATTCTCC	TGCCTCAGCC	TCCCAAGTAG	CTGGGATTAC	AGGCACGTGC
6551	CACCACACCC	AGCTAATATT	TGTATGGATG	GTCTCAATCT	CCTGACCTCG
6601	TGATTTGTAT	GGATGGTCTC	GATCTGACCT	CATGATCCGC	CTGCCTGGGC
6651	CTCCCAAAGT	GCTGGGATTA	CAGGCGTGAG	CCACTGTGCC	CGGCCGACAT
6701	AGAATGTTTA	CATCATTGCA	GAAAGTTTCT	GCAGGAAGAG	CCTAGAAGGA

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)	
6751	GAAAGCCTAG AATCATGATA AAATTGCAGA TATCTTTGCT TATCCCTGTC
Exon C5	
6801	CCCTTCCAGG <u>TCTGTCCCA ACAGGCACCA CACCGGGTG GACTCCCTGT</u>
6851	<u>GTAATTCTC GCCACTGGCT CGGAGAGTAG ACAGAGTTGC CATCTATGAG</u>
6901	<u>GAATTTCTGC GGATGACCCG GAATGGTACC CAGCTGCAGA ACTTCACCCT</u>
6951	<u>GGACAGGAGC AGTGTCTTG TGGATGGTAA AGCTCCCTGG GTCATTGGGA</u>
7001	CTGAGGTGGA AGCTCCCACT TCCTCACCTG GGTCTTCCC TGGGAATCTG
7051	AAGGCTTGGG GTTGATTCTG CATCGAGCTT TCTCAGACTG GGAGAAAGTG
7101	GCTTAGTTCT CCTAAGCTTT ACCCATCATT GAAGGAAAGA AAAGGACGCC
7151	CGAGGGATAT GGGAGGCATT TGCCCTCTTC TGGCCAGCTC TGTGACCTCA
7201	GGCTAGTCAC ATCTCCTTTC TGGACTTCTT ATCTCTCTGT ACTTAGCAAG
7251	CCACTTGGTT TTTGGTTCCC ATCTTGCCTG CCCTAGATGG TATTGCTCCT
7301	CCACCCCAG GCAGCTGCAG TGTAAACAA TTACCCTGAT TAGTTATTGT
7351	TGTTGTGTTG TTTGTTTGT TTTGAGACAG GGTCTCACTC TGTCACCTAG
7401	GCTGGAGTGC AGTGACATGA TCTCAGCTCA CTGCAACCTC AACCCCTGGA
7451	CTCAAGCAAT CCACCCACTT CAGCCTCCCA AGTAACTGGG ACTACAGCCA
7501	TGCGCCACCA CACCCGATA ATTTTGTAT TTTTCTAGA GATGGGGTTT
7551	TGCAACATTG CCCAGGCTGG TCTTGAATC CTGAGCTCAA GCATGCCACC
7601	TGCTTCAGCC TCCCAAAGTG CTGGGATTAC AGGCAGGCAG GCACCACTGC
7651	AGCTGGTTCT GGTTTTTGT GTTTGTTTTT TTCTTTTAGA GGCAGGGTCT
7701	CGCTCTGTTA ACCAGAATGG AGTACAGTGG TGCAATCATA GCTCACTGCA
7751	GTCTTGAACCT CCTGGGCTCA AGCGATCCTC CCACCTCAGC CTCCTGAGTA
7801	CCTGGAACTA CAGGCACGTG TCACCACGCC TTGCTAATTT CTAAATTTTT
7851	TGTAGAGACA GGGTCTCACT ATGTTGCCCA GACTGGTCTC TAATTCCTGG

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
7901	CCACAAGTGA	TCCTCCTGCC	TCAGCAGGTC	AATGAGGGCT	TCCAGTTTCA
7951	AGTTGTATGT	GATTCATCCT	CAACAAATGT	GGTAGGATGG	ACCTATTTTC
8001	CAACTCCAGA	GATGGCTTCA	AGGTGGCTCA	ACTTTGCATA	TCCAATTTTA
8051	CCCATTCAAA	GAATAGTTAT	ATACATTGTA	CCATGTATCA	GGAATATAAC
8101	AGAGAGTAAC	TGTTTGCTCT	TTCACCACTA	TATTCCAAGA	ACCCCATATT
8151	CTGCCTGGCA	CATAATAAAC	ACTCAAGTCA	TATTTGCAGA	AGGAATAACT
8201	AGATTTCATA	CAAGGTTCTT	TTCAAGTCAA	ATGCGAATAA	CGTTTTAGAC
8251	GGGACCTTCC	AATGCCTGTG	TGCACTGTCC	TTGATTCCGA	ATTATTGTTG
8301	TGCAAGAGAG	CACTGTTGAT	CCTTCAGAAT	CAACAAGCCT	TTCACATGCC
8351	TGTCACAGGT	TTTTCTTTTT	CTTGTTTTAC	CAATTTTGT	TGTTGTTTGT
8401	TTGTTGTTAT	TGTTTTGTTT	TGTTTTTGTT	TTTTATTGT	TTTTATTTTT
8451	TCTTTTTTTT	TGAGACAGAG	TCTCGCTCTG	TCACCCAGGC	TGGAGTGCAG
8501	TGGCAGCATC	TCCGCCCACT	GCAAGCTCCG	CCTCCTGGGT	TCATGCCATT
8551	TTCCTGCCTC	AGCCTCCTGA	GTAGCTGGGA	CTACAGGCGC	CTGCCACCAT
8601	GTCTGGCTAA	TTTTTTTTGT	ATTTTITAGTA	GAAACAGGGT	TTCACCATGT
8651	TGACCAGGAT	GGTCTCGATC	TCCTGACCTC	GTGATCTGCC	CACCTGGGCC
8701	TCCCAAAGTG	CTGGGATTAC	AGGCGTGAGC	CACCACACCC	AGCCCCAATT
8751	TTTTTTTTTAA	TTAAAATTGT	TGTCAGCTCA	CAAGCTTTCT	AAAAACAGGC
8801	CATGGACCCA	GCATCGCTGT	AGTTTGCCAA	ACCCTTGCTT	TGAATCAGTA
8851	CCATCCAATA	GAACTTTCTG	CAGTGATAGA	AAATGTTTCT	ATCTGTGCTA
8901	TTCAGCACAA	AGCCATGTGT	GATTACTAAG	CTTGAAGTGT	GGTTAATGTA
8951	ACTGAGATAC	CGAAGTTTTA	ATTTTATTTA	ATTTTAATTT	AAAAAGCCAC
9001	TTGTGGCTGC	TCCATATTGC	ACACTACTTT	TTAAAATTAT	TATTTGTATA
9051	TATTTAAGGG	GCACAAGTAC	AATTTTGTTG	CATGGATTTA	TAGCCAGTG

Table 3 (continued)

Genomic Carboxy Terminal (SEQ ID NO: 3)					
9101	GGGAAGTCTG	GGCTTTTAGG	GTATCTATTA	CCTGAATAAT	GTACATTGTA
9151	CCCATTGAGT	AATTTCTCAT	CATCCACTCT	CCTCCACTCC	CCAACCCCTC
9201	CAAGTTTCCA	CTGTCTATTA	TTCCACTCTC	TATGTCCATG	CCTATGCATT
9251	ATTTAGCATT	GACATGTCTA	TGCATTATTT	AGTCAAATAC	ATGTGCTATT
9301	TGACTTCCTG	TATCTGAGTT	GTTTGACTTA	AGATAATGAC	CTTCACTTGC
9351	ATCCATGTTG	CTGCAAAAGA	CATGATTTCA	TTCTTTTTTA	TGCCTGGGTG
9401	GTATTGCATT	GTGTGTGTGT	GTGTGTGTGT	GTGTGTAGAG	AGAGAGAGAG
9451	ATCACATTTT	CTTTATACAG	TCCTCCATTG	ATGGGCACTT	AGGTTGATTG
9501	CATATCTTTG	CTATTGTGAA	TAGTTTGTGT	ATAAACACAC	AGGTTGAGGT
9551	GTCTTTTTGA	CAAATTATT	TATTTTCCTT	TGTGTAGATA	CCCAGTCGTG
9601	GGATTCCTGG	ATCAAATGGT	AGTTTCATTT	TTAGTTATTT	GAGAAATCTC
9651	CACGTTTTTC	ATAGAGATTA	TACTAAATTA	CATTCCCACC	AACAGTGTGT
9701	AACGGTTCAC	TTTTCTTGCA	TCCTTTTTAA	CATCTGTTAT	TTTTGTCTTT
9751	TTAGTAACAG	CCATTCTGAC	TGGCGTAAGG	TGGTATCTCA	TCATGGTTTT
9801	AATCTGTATT	TCTCTGATTA	TTAGTAATGT	CGAGCATTTT	TTCATATGCT
9851	TGTTAGCCAT	TGGTATGTCT	TCTACATCTT	TAAGAAGCTG	GCTATGGGCT
9901	GGGCGCAGTG	GCTCACACCT	GTAATCCCAG	CAC'TTTGGGA	GGCCGAGGCA
9951	GGCGGATCAC	GAGGTCAGGA	GTTAAAAACC	AGCCTGGCCA	ACATGGTAAA
10001	ACCCTGCCTC	TACTAAAAAT	ACAAAAAATT	ACCCAGGCAT	GGTGGTGCGC
10051	CTGTAATCCC	AGCTACTCAG	GAAGCTGAGG	CAGGAGAATC	ACTTGAACCC
10101	AGGAGGCGGA	GGTTGCAGTG	AGACGAGATC	ACATCATTGC	ACTCCAGCCT
10151	GGGTGACAGA	GTGAGACTCT	ATCTTGAGAA	AAAAAAAAG	TTGGCTATAA
10201	CAGGGTTGTA	GAAGTAGAGG	AACCAGTAAC	CCTTCTCGCC	ATGCCTGATG
10251	ATGGCTTTAC	ATCCCTGTCT	TCATGGAGTT	TATGCTGTCTG	TGAGGAATAA

Table 3 (continued)

Genomic Carboxy Terminal
(SEQ ID NO: 3)

10301 CAAGAACAGG CAGTTGTCAA TTATAAATTA TTTGATGTGA ACCTATTCAT
 10351 ACATGGGTGT GGTCA TCAGG GAAGGCTTCC TGGAGGAAAT GACATTGAAG
 10401 GTGAATTCTA AAAGATGACG ATAAACCACC AAGTGAAGGA GAGCTTAAAT
 10451 GTGTTTTTAG GCAGAAGAAA AACCTTTTGG GTGAAAATTT TAAAACTTAG
 10501 AGAGGTCCCA TCAGTTTCCA ACTGCGATGA TCCATTCTCT CCACCACTGC
 10551 CCTTGGGCCC AGCCCAATTT AGGTCCACCA TGCCCAGAGG CATGAATTTA
 10601 ACTTATGACA CTCTTG TGGT GGAATAATGG CTTTGGGCTT ATGTAGCCAT
 10651 GTGTCATTTT TTTAGAGATA CAAATTGAAA TATTTGGGGT GAGATGTCAT
 10701 GGTGTCTACT GGCCTCTAAA ACTTCAGTGA AAACATTTAC TTTCCTGAA
 10751 ATGTCAATAA ATCATAAATT GGATGTATAT GTTTTAGTTG GAGGAAATAT
 10801 AAACCACTAA ATCTAGGTGA TGCATATTTA TTATACTCTT CTCTCTGCTT
 10851 TTTTGTACGC TTGTAAAATT GTATTTAAAA GAATAAGACA CACTTGGCCG
 10901 GGC GCGGTGG CTCACGCCTG TAATCCCAGC ACTTTGGGAG ACCGAGGTGG
 10951 GTGGATCATG AGGTCAGGAG TTCAAGACCA GCCTGGCCAA CATGGTAAAA
 11001 CTCCATCACT ACATACAAAA ATTAGCCAGG CATTTTGGCG GGCACCTGTA
 11051 ATCTCAGCTA CTTGGGAGGC TGAAGCAGGA GAATTGCTTG AACCCGGGAA
 11101 GCAGAGGTTG CAGTGAGCCA AGATCACGCC ACTGCACTCT AGCCTGGGCA
 11151 ACAGAGCAAG ACTCCATCTC CAGAAAAAAA AAAAAAAAAA GACACACTCA

Exon C6

11201 CATGCACCCT CCATTTCTTT CATTTCTAGG GTATTCTCCC AACAGAAATG
 11251 AGCCCTTAAC TGGAATTCT GGTAAGTCTC AAAGAAGCCC CAGCCCAGGG
 11301 TAGGGAGGGG GTAGCCTGAT GGTGCTTTGC CTTGTCCAAG AGCACCAGGC
 11351 ACACAGAGTC TTGGATGAGG ATCAAATTG CCAACCCATG GCAAAGACTA
 11401 TTGAGGCATA GTAAAGGGAT AGCAGGGATC CTGGCTTTCT GGGGGCCCAG

Table 3 (continued)

Genomic Carboxy Terminal
(SEQ ID NO: 3)

11451 TTTTGGGGG CATCAGAGGC ATGAGGTGTT GAGCCACTAA GCTCTCTTCC

11501 CCAGGGGCTG TGCCCATCCT CAGGCCACAT AGGGTCCAAG AAGGAGCCCT

Exon C7

11551 GGGACGTGGC AGGAGGTGGC TCACCCAGC CCTTGTCTCC CCAGACCTTC

11601 CCTTCTGGGC TGTATCCTC ATCGGCTTGG CAGGACTCCT GGGAGTCATC

11651 ACATGCCTGA TCTGCGGTGT CCTGGTGAGC AAGGAAGGGT TGCTTGTCTT

11701 CTTAACAATT GGGTTGTAAG AGTTCTTAAT ATATTATAAA ACCATACTAT

11751 ACTATACACA AGTCCTTTGC TGGATATATG TTTTGCAAAT ATTTTCTCCC

11801 AGTTCACGGA GTGGCTTTCC TATTTTCTTT TTATAATTTT ATTTTAAATT

11851 AATTGACAAA TAATGAATGC ATATATTTAG GGGATACAAT GTGATGCTTT

11901 GGTATATGTA CAATTATGGA ATGACTCAAT CAAGCTAATT AATATGTCCC

11951 TCACCTCTCA TACTTATTAT TTCTTTGTGG TGTGAACATT GGCAACCTAT

12001 ACTCTTAGCA ATTTTGAAAT CTACATTATT ATTAACATA GTTACTATGT

12051 TATGCAGATC TCAAAAACCT CACAACCTAT ATGCTGATTA CAAGATATTG

12101 AGAGAAAAAG TGATTGCAAA GAGTGTAAT AAAATAATGT AAGAGGGAAA

12151 AATGTAACAA AATTAGTCGT TAGGGAAATG TACACGGAAG TCACAATGAG

12201 AGGCCACTTT TCACAAGAAT GGATAAAATT GAAAAGATTG ACTATAACAA

12251 GTGTTGGTGA AAATGTGACA GAACTGGAAC TCTCATAAAG TGAAAGTGGA

12301 AAATAGCTTG GCCATTTCTT TGAAAATTAC ACACACCTAC CGTAAGACCT

12351 ACCATCCAC TACTAGTAAT TTATCTAAGA GAAATAAAAA CATATGTCTA

12401 TATGAAGACT TGTACACAAG TAAATGTTCA TAACAGCTTT GTTTGTAATA

Table 3 (continued)

		Genomic Carboxy Terminal (SEQ ID NO: 3)				
12451	GCCAAACTCT	GAAAACAAGC	CCCTAATGTC	CATTAACAAA	TATATCCTGA	
12501	CAATGGAATA	TTATTTCAGCA	ACAAAAAGGA	ATTATTAATA	CATTAATAAA	
12551	TTATACAGCA	ACATGTATAA	ATTGCAAAAT	AGTTATGCCT	AGTGAAAGAA	
12601	TCCAGATGAA	GAAAAGAGTA	CATGCCATAT	GATTCCCTTA	ATAGACAAAT	
12651	TCTAGAAAAT	ACAAACTAAT	CTGTAAGGAC	AGGAATCAGA	TCAGCGGTTG	
12701	CCTGGGAATG	AAAATGTGTT	TGCAGTGGCA	GGGAAAAAGG	AATTGTAAAA	
12751	GAGCAGGAAG	AAAGTTTTTT	TGTTGTTTTT	TTTTTGTTTT	TTCTTGAGAC	
12801	AGAGTCTTAG	TCTATCGCCC	AAGCTGGAGT	GCAATGGCAC	GATCTCAGCT	
12851	CATTGCAACC	TCTGCCTCTC	GGGTTCAAGC	GTTTTTCCTG	CCCCAGCCTC	
12901	CCAAGTAGCT	GGGATTACAC	ATGCGCACCA	CCACACTCAG	CTAATTTTTG	
12951	TATTTTTAGT	AGAGACGGGG	TTTTACCATG	TTGGCCAGGC	TGGTCTCGAA	
13001	CTCCTGACCT	CAGGTGATCC	ACCCGCCTTG	GCCTCCCAA	GTGCTGGGAT	
13051	TACAGGAGTG	AGCCACCATG	CCTGGCCAGG	ACGAAAGTTT	TGGGGATGAT	
13101	GGATGGATGT	TCCTTATGTT	GATTGTGGTG	ACGATTCAAT	AAGTTATGAT	
13151	CAGAACTTAT	CAAAACATTC	ACTTTAAATG	TGTGCAGTTT	ATTTTATGTC	
13201	AGTTATGCCT	CAGTTAAGCT	GGACAGATGT	AGAGGAGGAA	GGGAGGGAGA	
13251	GAGGGGGCTG	AGATCAGGAC	CAAAGCCAG	AGAGAAAGAG	ACTGAGAATG	
13301	AGATGAGAGA	GAAATGGTAT	TTAGACAGAA	GACAGGCGAT	AGATGATTGA	
13351	TAGTTGACAG	ATGATTGGTG	GATANNNNNN	NNNNNNNNNN	NNNNNNNNNN	
13401	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	

Table 3 (continued)

Genomic Carboxy Terminal
(SEQ ID NO: 3)

13451 NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN
 13501 AGGAGGTTTA AACAAAACGC AATTATGTTG AAATGACAAT GATTGTGGAT
 13551 ATAAAGGTAG ATAGAAATAG ATATTTGTGA AGATAATGGT TAGATAAAAA
 13601 TGATAGGTAA CAGATATTGA TAGATCTTGA TAAGTAGATG ATAAATACAT
 13651 GATTGATGGA TGACAGGTGA TTGATAGATG ATTTGATGGA TTATAAATAG
 13701 GAGATGATTG AGAGGTGAGA GATAATTGAT GGTATTATTGA TTGGTAGATA
 13751 ATTGATTGAC AGGTTGATAA ATATTGATAG CTAGATGATA GATAAATAGA
 13801 TCATTGGTAG ATATGTGATA TATTGATAAA GAAATTCAGA GGCAAAAGGA
 13851 GAGAGAAATG AAGGGGATAT CGGAGGGGGA AAAATTTTTT TAAACCGAGA
 13901 GTGAAACAAG GAGACAGAAG AAAAGAAAGT GGTGAAAAGA GGAAAAGAAC
 13951 TGAGGGAGAA ATTAAATGAA ACAATGAAGG GAGACAGAGG AAGCATAAGG

Exon C8

14001 CCTCTGGCTT TGGCCATATT CTCACCCCTG TGGTCTCCTC TCCCTGGACG
 14051 GCTGACCAGT CCATTCTCAC GCCTCCTCCT CACCCTCATA GGTGACCACC
 14101 CGCCGGCGGA AGAAGGAAGG AGAATACAAC GTCCAGCAAC AGTGCCAGG
 14151 CTACTACCAG TCACACCTAG ACCTGGAGGA TCTGCAATGA CTGGAACCTG
 14201 CCGGTGCCTG GGGTGCCTTT CCCCAGCCA GGGTCCAAAG AAGCTTGGCT
 14251 GGGGCAGAAA TAAACCATAT TGGTCGG

Table 4

Human cDNA of CA125 (SEQ ID NO: 4)					
1	AAGCGTTGCA	CAATTCCCCC	AACCTCCATA	CATACGGCAG	CTCTTCTAGA
51	CACAGGTTTT	CCCAGGTCAA	ATGCGGGGAC	CCCAGCCATA	TCTCCCACCC
101	TGAGAAATTT	TGGAGTTTCA	GGGAGCTCAG	AAGCTCTGCA	GAGGCCACCC
151	TCTCTGAGGG	GATTCTTCTT	AGACCTCCAT	CCAGAGGCAA	ATGTTGACCT
201	GTCCATGCTG	AAACCCTCAG	GCCTTCCTGG	GTCATCTTCT	CCCACCCGCT
251	CCTTGATGAC	AGGGAGCAGG	AGCACTAAAG	CCACACCAGA	AATGGATTCA
301	GGACTGACAG	GAGCCACCTT	GTCACCTAAG	ACATCTACAG	GTGCAATCGT
351	GGTGACAGAA	CATACTCTGC	CCTTTACTTC	CCCAGATAAG	ACCTTGGCCA
401	GTCCTACATC	TTCGGTTGTG	GGAAGAACCA	CCCAGTCTTT	GGGGGTGATG
451	TCCTCTGCTC	TCCCTGAGTC	AACCTCTAGA	GGAATGACAC	ACTCCGAGCA
501	AAGAACCAGC	CCATCGCTGA	GTCCCCAGGT	CAATGGAACT	CCCTCTAGGA
551	ACTACCCTGC	TACAAGCATG	GTTTCAGGAT	TGAGTTCCCC	AAGGACCAGG
601	ACCAGTTCCA	CAGAAGGAAA	TTTTACCAA	GAAGCATCTA	CATACACACT
651	CACTGTAGAG	ACCACAAGTG	GCCCAGTCAC	TGAGAAGTAC	ACAGTCCCCA
701	CTGAGACCTC	AACAAC TGAA	GGTGACAGCA	CAGACCUC	CTGGGACACA
751	AGATATATTC	CTGTAAAAAT	CACATCTCCA	ATGAAAACAT	TTGCAGATTC
801	AACTGCATCC	AAGGAAAATG	CCCCAGTGTC	TATGACTCCA	GCTGAGACCA
851	CAGTTACTGA	CTCACATACT	CCAGGAAGGA	CAAACCCATC	ATTTGGGACA
901	CTTTATTCTT	CCTTCCTTGA	CCTATCACCT	AAAGGGACCC	CAAATTCAG
951	AGGTGAAACA	AGCCTGGAAC	TGATTCTATC	AACCACTGGA	TATCCCTTCT
1001	CCTCTCCTGA	ACCTGGCTCT	GCAGGACACA	GCAGAATAAG	TACCAGTGCG
1051	CCTTTGTCAT	CATCTGCTTC	AGTTCTCGAT	AATAAAATAT	CAGAGACCAG
1101	CATATTCTCA	GGCCAGAGTC	TCACCTCCCC	TCTGTCTCCT	GGGGTGCCCG
1151	AGGCCAGAGC	CAGCACAATG	CCCAACTCAG	CTATCCCTTT	TTCCATGACA
1201	CTAAGCAATG	CAGAAACAAG	TGCCGAAAGG	GTCAGAAGCA	CAATTCCTC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

1251	TCTGGGGACT	CCATCAATAT	CCACAAAGCA	GACAGCAGAG	ACTATCCTTA
1301	CCTTCCATGC	CTTCGCTGAG	ACCATGGATA	TACCCAGCAC	CCACATAGCC
1351	AAGACTTTGG	CTTCAGAATG	GTTGGGAAGT	CCAGGTACCC	TTGGTGGCAC
1401	CAGCACTTCA	GCGCTGACAA	CCACATCTCC	ATCTACCACT	TTAGTCTCAG
1451	AGGAGACCAA	CACCCATCAC	TCCACGAGTG	GAAAGGAAAC	AGAAGGAACT
1501	TTGAATACAT	CTATGACTCC	ACTTGAGACC	TCTGCTCCTG	GAGAAGAGTC
1551	CGAAATGACT	GCCACCTTGG	TCCCCACTCT	AGGTTTTACA	ACTCTTGACA
1601	GCAAGATCAG	AAGTCCATCT	CAGGTCTCTT	CATCCCACCC	AACAAGAGAG
1651	CTCAGAACCA	CAGGCAGCAC	CTCTGGGAGG	CAGAGTTCCA	GCACAGCTGC
1701	CCACGGGAGC	TCTGACATCC	TGAGGGCAAC	CACTTCCAGC	ACCTCAAAAG
1751	CATCATCATG	GACCAGTGAA	AGCACAGCTC	AGCAATTTAG	TGAACCCAG
1801	CACACACAGT	GGGTGGAGAC	AAGTCCTAGC	ATGAAAACAG	AGAGACCCCC
1851	AGCATCAACC	AGTGTGGCAG	CCCCTATCAC	CACTTCTGTT	CCCTCAGTGG
1901	TCTCTGGCTT	CACCACCCTG	AAGACCAGCT	CCACAAAAGG	GATTTGGCTT
1951	GAAGAAACAT	CTGCAGACAC	ACTCATCGGA	GAATCCACAG	CTGGCCCCAAC
2001	CACCCATCAG	TTTGCTGTTC	CCACTGGGAT	TTCAATGACA	GGAGGCAGCA
2051	GCACCAGGGG	AAGCCAGGGC	ACAACCCACC	TACTCACCAG	AGCCACAGCA
2101	TCATCTGAGA	CATCCGCAGA	TTTGACTCTG	GCCACGAACG	GTGTCCCAGT
2151	CTCCGTGTCT	CCAGCAGTGA	GCAAGACGGC	TGCTGGCTCA	AGTCCTCCAG
2201	GAGGGACAAA	GCCATCATAT	ACAATGGTTT	CTTCTGTCAT	CCCTGAGACA
2251	TCATCTCTAC	AGTCCTCAGC	TTTCAGGGAA	GGAACCAGCC	TGGGACTGAC
2301	TCCATTAAAC	ACTAGACATC	CCTTCTCTTC	CCCTGAACCA	GACTCTGCAG
2351	GACACACCAA	GATAAGCACC	AGCATTCCTC	TGTTGTCATC	TGCTTCAGTT
2401	CTTGAGGATA	AAGTGTGAGC	GACCAGCACA	TTCTCACACC	ACAAAGCCAC
2451	CTCATCTATT	ACCACAGGGA	CTCCTGAAAT	CTCAACAAAG	ACAAAGCCCA

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
2501	GCTCAGCCGT	TCTTTCCTCC	ATGACCCTAA	GCAATGCAGC	AACAAGTCCT
2551	GAAAGAGTCA	GAAATGCAAC	TTCCCCTCTG	ACTCATCCAT	CTCCATCAGG
2601	GGAAGAGACA	GCAGGGAGTG	TCCTCACTCT	CAGCACCTCT	GCTGAGACTA
2651	CAGACTCACC	TAACATCCAC	CCAACTGGGA	CACTGACTTC	AGAATCGTCA
2701	GAGAGTCCTA	GCACTCTCAG	CCTCCCAAGT	GTCTCTGGAG	TCAAACCAC
2751	ATTTTCTTCA	TCTACTCCTT	CCACTCATCT	ATTTACTAGT	GGAGAAGAAA
2801	CAGAGGAAAC	TTCGAATCCA	TCTGTGTCTC	AACCTGAGAC	TTCTGTTTCC
2851	AGAGTAAGGA	CCACCTTGGC	CAGCACCTCT	GTCCCTACCC	CAGTATTCCC
2901	CACCATGGAC	ACCTGGCCTA	CACGTTCAGC	TCAGTTCTCT	TCATCCCACC
2951	TAGTGAGTGA	GCTCAGAGCT	ACGAGCAGTA	CCTCAGTTAC	AAACTCAACT
3001	GGTTCAGCTC	TTCCTAAAT	ATCTCACCTC	ACTGGGACGG	CAACAATGTC
3051	ACAGACCAAT	AGAGACACGT	TTAATGACTC	TGCTGCACCC	CAAAGCACAA
3101	CTTGGCCAGA	GACTIONTCCC	AGATTCAAGA	CAGGGTTACC	TTCAGCAACA
3151	ACCACTGTTT	CAACCTCTGC	CACTTCTCTC	TCTGCTACTG	TAATGGTCTC
3201	TAAATTCACT	TCTCCAGCAA	CTAGTTCCAT	GGAAGCAACT	TCTATCAGGG
3251	AACCATCAAC	AACCATCCTC	ACAACAGAGA	CCACGAATGG	CCCAGGCTCT
3301	ATGGCTGTGG	CTTCTACCAA	CATCCCAATT	GGAAAGGGCT	ACATTACTGA
3351	AGGAAGATTG	GACACAAGCC	ATCTGCCCAT	TGGAACCACA	GCTTCCTCTG
3401	AGACATCTAT	GGATTTTACC	ATGGCCAAAG	AAAGTGCTCT	AATGTCAGTA
3451	TCTCCATCTC	AGTCCATGGA	TGCTGCTGGC	TCAAGCACTC	CAGGAAGGAC
3501	AAGCCAATTC	GTTGACACAT	TTTCTGATGA	TGTCTATCAT	TTAACATCCA
3551	GAGAAATTAC	AATACCTAGA	GATGGAACAA	GCTCAGCTCT	GACTCCACAA
3601	ATGACTGCAA	CTCACCTCC	ATCTCCTGAT	CCTGGCTCTG	CTAGAAGCAC
3651	CTGGCTTGGC	ATCTTGTCCT	CATCTCCTTC	TTCTCCTACT	CCCAAAGTCA
3701	CAATGAGCTC	CACATTTTCA	ACTCAGAGAG	TCACCACAAG	CATGATAATG

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
3751	GACACAGTTG	AAACTAGTCG	GTGGAACATG	CCCAACTTAC	CTTCCACGAC
3801	TTCCCTGACA	CCAAGTAATA	TTCCAACAAG	TGGTGCCATA	GGAAAAAGCA
3851	CCCTGGTTCC	CTTGGACACT	CCATCTCCAG	CCACATCATT	GGAGGCATCA
3901	GAAGGGGGAC	TTCCAACCCCT	CAGCACCTAC	CCTGAATCAA	CAAACACACC
3951	CAGCATCCAC	CTCGGAGCAC	ACGCTAGTTC	AGAAAGTCCA	AGCACCATCA
4001	AACTTACCAT	GGCTTCAGTA	GTAAAACCTG	GCTCTTACAC	ACCTCTCACC
4051	TTCCCCCTCAA	TAGAGACCCA	CATTCATGTA	TCAACAGCCA	GAATGGCTTA
4101	CTCTTCTGGG	TCTTCACCTG	AGATGACAGC	TCCTGGAGAG	ACTAACACTG
4151	GTAGTACCTG	GGACCCCACC	ACCTACATCA	CCACTACGGA	TCCTAAGGAT
4201	ACAAGTTCAG	CTCAGGTCTC	TACACCCAC	TCAGTGAGGA	CACTCAGAAC
4251	CACAGAAAAC	CATCCAAAGA	CAGAGTCCGC	CACCCCAGCT	GCTTACTCTG
4301	GAAGTCCTAA	AATCTCAAGT	TCACCCAATC	TCACCAGTCC	GGCCACAAAA
4351	GCATGGACCA	TCACAGACAC	AACTGAACAC	TCCACTCAAT	TACATTACAC
4401	AAAATTGGCA	GAAAAATCAT	CTGGATTTGA	GACACAGTCA	GCTCCAGGAC
4451	CTGTCTCTGT	AGTAATCCCT	ACCTCCCCTA	CCATTGGAAG	CAGCACATTG
4501	GAACTAACTT	CTGATGTCCC	AGGGGAACCC	CTGGTCCTTG	CTCCCAGTGA
4551	GCAGACCACA	ATCACTCTCC	CCATGGCAAC	ATGGCTGAGT	ACCAGTTTGA
4601	CAGAGGAAAT	GGCTTCAACA	GACCTTGATA	TTTCAAGTCC	AAGTTCACCC
4651	ATGAGTACAT	TTGCTATTTT	TCCACCTATG	TCCACACCTT	CTCATGAACT
4701	TTCAAAGTCA	GAGGCAGATA	CCAGTGCCAT	TAGAAATACA	GATTCAACAA
4751	CGTTGGATCA	GCACCTAGGA	ATCAGGAGTT	TGGGCAGAAC	TGGGGACTTA
4801	ACAACTGTTC	CTATCACCCC	ACTGACAACC	ACGTGGACCA	GTGTGATTGA
4851	ACACTCAACA	CAAGCACAGG	ACACCCTTTC	TGCAACGATG	AGTCCTACTC
4901	ACGTGACACA	GTCACTCAAA	GATCAAACAT	CTATACCAGC	CTCAGCATCC
4951	CCTTCCCATC	TTACTGAAGT	CTACCCTGAG	CTCGGGACAC	AAGGGAGAAG

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

5001	CTCCTCTGAG	GCAACCACTT	TTTGGAACC	ATCTACAGAC	ACACTGTCCA
5051	GAGAGATTGA	GACTGGCCCA	ACAAACATTC	AATCCACTCC	ACCCATGGAC
5101	AACACAACAA	CAGGGAGCAG	TAGTAGTGGA	GTCACCCTGG	GCATAGCCCA
5151	CCTTCCCATA	GGAACATCCT	CCCCAGCTGA	GACATCCACA	AACATGGCAC
5201	TGGAAAGAAG	AAGTTCTACA	GCCACTGTCT	CTATGGCTGG	GACAATGGGA
5251	CTCCTTGTTA	CTAGTGCTCC	AGGAAGAAGC	ATCAGCCAGT	CATTAGGAAG
5301	AGTTTCCTCT	GTCCTTTCTG	AGTCAACTAC	TGAAGGAGTC	ACAGATTCTA
5351	GTAAGGGAAG	CAGCCCAAGG	CTGAACACAC	AGGGAAATAC	AGCTCTCTCC
5401	TCCTCTCTTG	AACCCAGCTA	TGCTGAAGGA	AGCCAGATGA	GCACAAGCAT
5451	CCCTCTAACC	TCATCTCCTA	CAACTCCTGA	TGTGGAATTC	ATAGGGGGCA
5501	GCACATTTTG	GACCAAGGAG	GTCACCACAG	TTATGACCTC	AGACATCTCC
5551	AAGTCTTCAG	CAAGGACAGA	GTCCAGCTCA	GCTACCCTTA	TGTCCACAGC
5601	TTTGGGAAGC	ACTGAAAATA	CAGGAAAAGA	AAACTCAGA	ACTGCCTCTA
5651	TGGATCTTCC	ATCTCCAAC	CCATCAATGG	AGGTGACACC	ATGGATTTCT
5701	CTCACTCTCA	GTAATGCCCC	CAATACCACA	GATTCATTG	ACCTCAGCCA
5751	TGGGGTGAC	ACCAGCTCTG	CAGGGACTTT	GGCCACTGAC	AGGTCATTGA
5801	ATACTGGTGT	CACTAGAGCC	TCCAGATTGG	AAAACGGCTC	TGATACCTCT
5851	TCTAAGTCCC	TGTCTATGGG	AAACAGCACT	CACACTTCCA	TGACTGACAC
5901	AGAGAAGAGT	GAAGTGTCTT	CTTCAATCCA	TCCCCGACCT	GAGACCTCAG
5951	CTCCTGGAGC	AGAGACCACT	TTGACTTCCA	CTCCTGGAAA	CAGGGCCATA
6001	AGCTTAACAT	TGCCTTTTTT	ATCCATTCCA	GTGGAAGAAG	TCATTTCTAC
6051	AGGCATAACC	TCAGGACCAG	ACATCAACTC	AGCACCCATG	ACACATTCTC
6101	CCATCACCCC	ACCAACAATT	GTATGGACCA	GTACAGGCAC	AATTGAACAG
6151	TCCACTCAAC	CACTACATGC	AGTTTCTTCA	GAAAAAGTTT	CTGTGCAGAC
6201	ACAGTCAACT	CCATATGTCA	ACTCTGTGGC	AGTGTCTGCT	TCCCCTACCC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

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6251  ATGAGAATTC AGTCTCTTCT GGAAGCAGCA CATCCTCTCC ATATTCCTCA
6301  GCCTCACTTG AATCCTTGGA TTCCACAATC AGTAGGAGGA ATGCAATCAC
6351  TTCCTGGCTA TGGGACCTCA CTACATCTCT CCCCACTACA ACTTGGCCAA
6401  GTACTAGTTT ATCTGAGGCA CTGTCCTCAG GCCATTCTGG GGTTCAAAC
6451  CCAAGTTCAA CTACGACTGA ATTTCCACTC TTTTCAGCTG CATCCACATC
6501  TGCTGCTAAG CAAAGAAATC CAGAAACAGA GACCCATGGT CCCCAGAATA
6551  CAGCCGCGAG TACTTTGAAC ACTGATGCAT CCTCGGTCAC AGGTCTTTCT
6601  GAGACTCCTG TGGGGGCAAG TATCAGCTCT GAAGTCCCTC TTCCAATGGC
6651  CATAACTTCT AGATCAGATG TTTCTGGCCT TACATCTGAG AGTACTGCTA
6701  ACCCGAGTTT AGGCACAGCC TCTTCAGCAG GGACCAAATT AACTAGGACA
6751  ATATCCCTGC CCACTTCAGA GTCTTTGGTT TCCTTTAGAA TGAACAAGGA
6801  TCCATGGACA GTGTCAATCC CTTTGGGGTC CCATCCAAC ACTAATACAG
6851  AAACAAGCAT CCCAGTAAAC AGCGCAGGTC CACCTGGCTT GTCCACAGTA
6901  GCATCAGATG TAATTGACAC ACCTTCAGAT GGGGCTGAGA GTATTCCCAC
6951  TGTCTCCTTT TCCCCCTCCC CTGATACTGA AGTGACAACT ATCTCACATT
7001  TCCCAGAAAA GACAACTCAT TCATTTAGAA CCATTTTCATC TCTCACTCAT
7051  GAGTTGACTT CAAGAGTGAC ACCTATTCCT GGGGATTGGA TGAGTTCAGC
7101  TATGTCTACA AAGCCACAG GAGCCAGTCC CTCCATTACA CTGGGAGAGA
7151  GAAGGACAAT CACCTCTGCT GCTCCAACCA CTTCCCCCAT AGTTCTCACT
7201  GCTAGTTTCA CAGAGACCAG CACAGTTTCA CTGGATAATG AACTACAGT
7251  AAAAACCTCA GATATCCTTG ACGCACGGAA AACAAATGAG CTCCCCTCAG
7301  ATAGCAGTTC TTCTTCTGAT CTGATCAACA CCTCCATAGC TTCTTCAACT
7351  ATGGATGTCA CTAAAACAGC CTCCATCAGT CCCACTAGCA TCTCAGGAAT
7401  GACAGCAAGT TCCTCCCCAT CTCTCTTCTC TTCAGATAGA CCCCAGGTTC
7451  CCACATCTAC AACAGAGACA AATACAGCCA CCTCTCCATC TGTTTCCAGT

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Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

7501	AACACCTATT	CTCTTGATGG	GGGCTCCAAT	GTGGGTGGCA	CTCCATCCAC
7551	TTTACCACCC	TTTACAATCA	CCCACCCTGT	CGAGACAAGC	TCGGCCCTAT
7601	TAGCCTGGTC	TAGACCAGTA	AGAACTTTCA	GCACCATGGT	CAGCACTGAC
7651	ACTGCCTCCG	GAGAAAATCC	TACCTCTAGC	AATTCTGTGG	TGACTTCTGT
7701	TCCAGCACCA	GGTACATGGG	CCAGTGTAGG	CAGTACTACT	GACTTACCTG
7751	CCATGGGCTT	TCTCAAGACA	AGTCCTGCAG	GAGAGGCACA	CTCACTTCTA
7801	GCATCAACTA	TTGAACCAGC	CACTGCCTTC	ACTCCCCATC	TCTCAGCAGC
7851	AGTGGTCACT	GGATCCAGTG	CTACATCAGA	AGCCAGTCTT	CTCACTACGA
7901	GTGAAAGCAA	AGCCATTCAT	TCTTCACCAC	AGACCCCAAC	TACACCCACC
7951	TCTGGAGCAA	ACTGGGAAAC	TTCAGCTACT	CCTGAGAGCC	TTTTGGTAGT
8001	CACTGAGACT	TCAGACACAA	CACTTACCTC	AAAGATTTTG	GTCACAGATA
8051	CCATCTTGTT	TTCAACTGTG	TCCACGCCAC	CTTCTAAATT	TCCAAGTACG
8101	GGGACTCTGT	CTGGAGCTTC	CTTCCCTACT	TTACTCCCGG	ACACTCCAGC
8151	CATCCCTCTC	ACTGCCACTG	AGCCAACAAG	TTCATTAGCT	ACATCCTTTG
8201	ATTCCACCCC	ACTGGTGACT	ATAGCTTCGG	ATAGTCTTGG	CACAGTCCCA
8251	GAGACTACCC	TGACCATGTC	AGAGACCTCA	AATGGTGATG	CACTGGTTCT
8301	TAAGACAGTA	AGTAACCCAG	ATAGGAGCAT	CCCTGGAATC	ACTATCCAAG
8351	GAGTAACAGA	AAGTCCACTC	CATCCTTCTT	CCACTTCCCC	CTCTAAGATT
8401	GTTGCTCCAC	GGAATACAAC	CTATGAAGGT	TCGATCACAG	TGGCACTTTC
8451	TACTTTGCCT	GCGGGAACTA	CTGGTTCCCT	TGTATTCACT	CAGAGTTCTG
8501	AAAACTCAGA	GACAACGGCT	TTGGTAGACT	CATCAGCTGG	GCTTGAGAGG
8551	GCATCTGTGA	TGCCACTAAC	CACAGGAAGC	CAGGGTATGG	CTAGCTCTGG
8601	AGGAATCAGA	AGTGGGTCCA	CTCACTCAAC	TGGAACCAAA	ACATTTTCTT
8651	CTCTCCCTCT	GACCATGAAC	CCAGGTGAGG	TTACAGCCAT	GTCTGAAATC
8701	ACCACGAACA	GACTGACAGC	TACTCAATCA	ACAGCACCCA	AAGGGATACC

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
8751	TGTGAAGCCC	ACCAGTGCTG	AGTCAGGCCT	CCTAACACCT	GTCTCTGCCT
8801	CCTCAAGCCC	ATCAAAGGCC	TTTGCCTCAC	TGACTACAGC	TCCCCCATCA
8851	ACTTGGGGGA	TCCCACAGTC	TACCTTGACA	TTTGAGTTTT	CTGAGGTCCC
8901	AAGTTTGGAT	ACTAAGTCCG	CTTCTTTACC	AACTCCTGGA	CAGTCCCTGA
8951	ACACCATTCC	AGACTCAGAT	GCAAGCACAG	CATCTTCCTC	ACTGTCCAAG
9001	TCTCCAGAAA	AAAACCCAAG	GGCAAGGATG	ATGACTTCCA	CAAAGGCCAT
9051	AAGTGCAAGC	TCATTTCAAT	CAACAGGTTT	TACTGAAACC	CCTGAGGGAT
9101	CTGCCTCCCC	TTCTATGGCA	GGGCATGAAC	CCAGAGTCCC	CAC TTCAGGA
9151	ACAGGGGACC	CTAGATATGC	CTCAGAGAGC	ATGTCTTATC	CAGACCCAAG
9201	CAAGGCATCA	TCAGCTATGA	CATCGACCTC	TCTTG CATCA	AAACTCACAA
9251	CTCTCTTCAG	CACAGGTCAA	GCAGCAAGGT	CTGGTTCTAG	TTCCTCTCCC
9301	ATAAGCCTAT	CCACTGAGAA	AGAAACAAGC	TTCCTTTCCC	CCACTGCATC
9351	CACCTCCAGA	AAGACTTCAC	TATTTCTTGG	GCCTTCCATG	GCAAGGCAGC
9401	CCAACATATT	GGTGCATCTT	CAGACTTCAG	CTCTGACACT	TTCTCCAACA
9451	TCCACTCTAA	ATATGTCCCA	GGAGGAGCCT	CCTGAGTTAA	CCTCAAGCCA
9501	GACCATTGCA	GAAGAAGAGG	GAACAACAGC	TGAAACACAG	ACGTTAACCT
9551	TCACACCATC	TGAGACCCCA	ACATCCTTGT	TACCTGTCTC	TTCTCCCACA
9601	GAACCCACAG	CCAGAAGAAA	GAGTTCTCCA	GAAACATGGG	CAAGCTCTAT
9651	TTTCTTCTCT	GCCAAGACCT	CCTTG GTTGA	AACAACTGAT	GGAACGCTAG
9701	TGACCACCAT	AAAGATGTCA	AGCCAGGCAG	CACAAGGAAA	TTCCACGTGG
9751	CCTGCCCCAG	CAGAGGAGAC	GGGGACCAGT	CCAGCAGGCA	CATCCCCAGG
9801	AAGCCCAGAA	GTGTCTACCA	CTCTCAAAAT	CATGAGCTCC	AAGGAACCCA
9851	GCATCAGCCC	AGAGATCAGG	TCCACTGTGC	GAAATTCTCC	TTGGAAGACT
9901	CCAGAAACAA	CTGTTCCCAT	GGAGACCACA	GTGGAACCAG	TCACCCTTCA
9951	GTCCACAGCC	CTAGGAAGTG	GCAGCACCAG	CATCTCTCAC	CTGCCCACAG

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
10001	GAACCACATC	ACCAACCAAG	TCACCAACAG	AAAATATGTT	GGCTACAGAA
10051	AGGGTCTCCC	TCTCCCCATC	CCCACCTGAG	GCTTGGACCA	ACCTTTATTC
10101	TGGAActCCA	GGAGGGACCA	GGCAGTCACT	GGCCACAATG	TCCTCTGTCT
10151	CCCTAGAGTC	ACCAACTGCT	AGAAGCATCA	CAGGGACTGG	TCAGCAAAGC
10201	AGTCCAGAAC	TGGTTTCAAA	GACAACTGGA	ATGGAATTCT	CTATGTGGCA
10251	TGGCTCTACT	GGAGGGACCA	CAGGGGACAC	ACATGTCTCT	CTGAGCACAT
10301	CTTCCAATAT	CCTTGAAGAC	CCTGTAACCA	GCCCAAATC	TGTGAGCTCA
10351	TTGACAGATA	AATCCAAACA	TAAAACCGAG	ACATGGGTAA	GCACCACAGC
10401	CATTCCCTCC	ACTGTCCTGA	ATAATAAGAT	AATGGCAGCT	GAACAACAGA
10451	CAAGTCGATC	TGTGGATGAG	GCTTATTCAT	CAACTAGTTC	TTGGTCAGAT
10501	CAGACATCTG	GGAGTGACAT	CACCCTTGGT	GCATCTCCTG	ATGTCACAAA
10551	CACATTATAC	ATCACCTCCA	CAGCACAAAC	CACCTCACTA	GTGTCTCTGC
10601	CCTCTGGAGA	CCAAGGCATT	ACAAGCCTCA	CCAATCCCTC	AGGAGGAAAA
10651	ACAAGCTCTG	CGTCATCTGT	CACATCTCCT	TCAATAGGGC	TTGAGACTCT
10701	GAGGGCCAAT	GTAAGTGCAG	TGAAAAGTGA	CCTTGCCCT	ACTGCTGGGC
10751	ATCTATCTCA	GACTTCATCT	CCTGCGGAAG	TGAGCATCCT	GGACGTAACC
10801	ACAGCTCCTA	CTCCAGGTAT	CTCCACCACC	ATCACCACCA	TGGGAACCAA
10851	CTCAATCTCA	ACTACCACAC	CCAACCCAGA	AGTGGGTATG	AGTACCATGG
10901	ACAGCACCCC	GGCCACAGAG	AGGCGCACAA	CTTCTACAGA	ACACCCTTCC
10951	ACCTGGTCTT	CCACAGCTGC	ATCAGATTCC	TGGACTGTCA	CAGACATGAC
11001	TTCAAACCTG	AAAGTTGCAA	GATCTCCTGG	AACAATTTCC	ACAATGCATA
11051	CAACTTCATT	CTTAGCCTCA	AGCACTGAAT	TAGACTCCAT	GTCTACTCCC
11101	CATGGCCGTA	TAAGTGTGAT	TGGAACCAGC	CTGGTCACTC	CATCCTCTGA
11151	TGCTTCAGCT	GTAAAGACAG	AGACCAGTAC	AAGTGAAAGA	ACATTGAGTC
11201	CTTCAGACAC	AACTGCATCT	ACTCCCATCT	CAACTTTTTTC	TCGTGTCCAG

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
11251	AGGATGAGCA	TCTCAGTTCC	TGACATTTTA	AGTACAAGTT	GGACTCCCAG
11301	TAGTACAGAA	GCAGAAGATG	TGCCTGTTTC	AATGGTTTCT	ACAGATCATG
11351	CTAGTACAAA	GACTGACCCA	AATACGCCCC	TGTCCACTTT	TCTGTTTGAT
11401	TCTCTGTCCA	CTCTTGACTG	GGACACTGGG	AGATCTCTGT	CATCAGCCAC
11451	AGCCACTACC	TCAGCTCCTC	AGGGGGCCAC	AACTCCCCAG	GAACCTCACTT
11501	TGGAAACCAT	GATCAGCCCCA	GCTACCTCAC	AGTTGCCCTT	CTCTATAGGG
11551	CACATTACAA	GTGCAGTCAC	ACCAGCTGCA	ATGGCAAGGA	GCTCTGGAGT
11601	TACTTTTTCA	AGACCAGATC	CCACAAGCAA	AAAGGCAGAG	CAGACTTTCCA
11651	CTCAGCTTCC	CACCACCACT	TCTGCACATC	CAGGGCAGGT	GCCCAGATCA
11701	GCAGCAACAA	CTCTGGATGT	GATCCACAC	ACAGCAAAAA	CTCCAGATGC
11751	AACTTTTTCAG	AGACAAGGGC	AGACAGCTCT	TACAACAGAG	GCAAGAGCTA
11801	CATCTGACTC	CTGGAATGAG	AAAGAAAAAT	CAACCCCAAG	TGCACCTTGG
11851	ATCACTGAGA	TGATGAATTC	TGTCTCAGAA	GATACCATCA	AGGAGGTTAC
11901	CAGCTCCTCC	AGTGTATTAA	AGGACCCTGA	ATACGCTGGA	CATAAACTTG
11951	GAATCTGGGA	CGACTTCATC	CCAAGTTTG	GAAAAGCAGC	CCATATGAGA
12001	GAGTTGCCCC	TTCTGAGTCC	ACCACAGGAC	AAAGAGGCAA	TTCACCCCTTC
12051	TACAAACACA	GTAGAGACCA	CAGGCTGGGT	CACAAGTTCC	GAACATGCTT
12101	CTCATTCAC	TATCCCAGCC	CACTCAGCGT	CATCCAAACT	CACATCTCCA
12151	GTGGTTACAA	CCTCCACCAG	GGAACAAGCA	ATAGTTTCTA	TGTCAACAAC
12201	CACATGGCCA	GAGTCTACAA	GGGCTAGAAC	AGAGCCTAAT	TCCTTCTTGA
12251	CTATTGAACT	GAGGGACGTC	AGCCCTTACA	TGGACACCAG	CTCAACCACA
12301	CAAACAAGTA	TTATCTCTTC	CCCAGGTTCC	ACTGCGATCA	CCAAGGGGCC
12351	TAGAACAGAA	ATTACCTCCT	CTAAGAGAAT	ATCCAGCTCA	TTCCTTGCCC
12401	AGTCTATGAG	GTCGTCAGAC	AGCCCCTCAG	AAGCCATCAC	CAGGCTGTCT
12451	AACTTTCCTG	CCATGACAGA	ATCTGGAGGA	ATGATCCTTG	CTATGCAAAC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

12501	AAGTCCACCT	GGCGCTACAT	CACTAAGTGC	ACCTACTTTG	GATACATCAG
12551	CCACAGCCTC	CTGGACAGGG	ACTCCACTGG	CTACGACTCA	GAGATTTACA
12601	TACTCAGAGA	AGACCACTCT	CTTTAGCAAA	GGTCCTGAGG	ATACATCACA
12651	GCCAAGCCCT	CCCTCTGTGG	AAGAAACCAG	CTCTTCCTCT	TCCCTGGTAC
12701	CTATCCATGC	TACAACCTCG	CCTTCCAATA	TTTTGTTGAC	ATCACAAGGG
12751	CACAGTCCCT	CCTCTACTCC	ACCTGTGACC	TCAGTTTTCT	TGTCTGAGAC
12801	CTCTGGCCTG	GGGAAGACCA	CAGACATGTC	GAGGATAAGC	TTGGAACCTG
12851	GCACAAGTTT	ACCTCCCAAT	TTGAGCAGTA	CAGCAGGTGA	GGCGTTATCC
12901	ACTTATGAAG	CCTCCAGAGA	TACAAAGGCA	ATTCATCATT	CTGCAGACAC
12951	AGCAGTGACG	AATATGGAGG	CAACCAGTTC	TGAATATTCT	CCTATCCCAG
13001	GCCATACAAA	GCCATCCAAA	GCCACATCTC	CATTGGTTAC	CTCCCACATC
13051	ATGGGGGACA	TCACTTCTTC	CACATCAGTA	TTTGGCTCCT	CCGAGACCAC
13101	AGAGATTGAG	ACAGTGTCTT	CTGTGAACCA	GGGACTTCAG	GAGAGAAGCA
13151	CATCCCAGGT	GGCCAGCTCT	GCTACAGAGA	CAAGCACTGT	CATTACCCAT
13201	GTGTCTAGTG	GTGATGCTAC	TACTCATGTC	ACCAAGACAC	AAGCCACTTT
13251	CTCTAGCGGA	ACATCCATCT	CAAGCCCTCA	TCAGTTTATA	ACTTCTACCA
13301	ACACATTTAC	AGATGTGAGC	ACCAACCCCT	CCACCTCTCT	GATAATGACA
13351	GAATCTTCAG	GAGTGACCAT	CACCACCCAA	ACAGGTCCTA	CTGGAGCTGC
13401	AACACAGGGT	CCATATCTCT	TGGACACATC	AACCATGCCT	TACTTGACAG
13451	AGACTCCATT	AGCTGTGACT	CCAGATTTTA	TGCAATCAGA	GAAGACCACT
13501	CTCATAAGCA	AAGGTCCCAA	GGATGTGACC	TGGACAAGCC	CTCCCTCTGT
13551	GGCAGAAACC	AGCTATCCCT	CTTCCCTGAC	ACCTTTCTTG	GTCACAACCA
13601	TACCTCCTGC	CACTTCCACG	TTACAAGGGC	AACATACATC	CTCTCCTGTT
13651	TCTGCGACTT	CAGTTCTTAC	CTCTGGACTG	GTGAAGACCA	CAGATATGTT
13701	GAACACAAGC	ATGGAACCTG	TGACCAATTC	ACCTCAAAAT	TTGAACAATC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

13751	CATCAAATGA	GATACTGGCC	ACTTTGGCAG	CCACCACAGA	TATAGAGACT
13801	ATTCATCCTT	CCATAAACAA	AGCAGTGACC	AATATGGGGA	CTGCCAGTTC
13851	AGCACATGTA	CTGCATTCCA	CTCTCCCAGT	CAGCTCAGAA	CCATCTACAG
13901	CCACATCTCC	AATGGTTCCT	GCCTCCAGCA	TGGGGGACGC	TCTTGCTTCT
13951	ATATCAATAC	CTGGTTCTGA	GACCACAGAC	ATTGAGGGAG	AGCCAACATC
14001	CTCCCTGACT	GCTGGACGAA	AAGAGAACAG	CACCCTCCAG	GAGATGAACT
14051	CAACTACAGA	GTCAAACATC	ATCCTCTCCA	ATGTGTCTGT	GGGGGCTATT
14101	ACTGAAGCCA	CAAAAATGGA	AGTCCCCTCT	TTTGATGCAA	CATTCATACC
14151	AACTCCTGCT	CAGTCAACAA	AGTCCCAGAG	TATTTTCTCA	GTAGCCAGCA
14201	GTAGACTTTC	AAACTCTCCT	CCCATGACAA	TATCTACCCA	CATGACCACC
14251	ACCCAGACAG	GGTCTTCTGG	AGCTACATCA	AAGATTCCAC	TTGCCTTAGA
14301	CACATCAACC	TTGGAAACCT	CAGCAGGGAC	TCCATCAGTG	GTGACTGAGG
14351	GGTTTGCCCA	CTCAAAAATA	ACCACTGCAA	TGAACAATGA	TGTCAAGGAC
14401	GTGTCACAGA	CAAACCCTCC	CTTTCAGGAT	GAAGCCAGCT	CTCCCTCTTC
14451	TCAAGCACCT	GTCCTTGTC	CAACCTTACC	TTCTTCTGTT	GCTTTCACAC
14501	CGCAATGGCA	CAGTACCTCC	TCTCCTGTTT	CTATGTCCTC	AGTTCTTACT
14551	TCTTCACTGG	TAAAGACCGC	AGGCAAGGTG	GATACAAGCT	TAGAAACAGT
14601	GACCAGTTCA	CCTCAAAGTA	TGAGCAACAC	TTTGGATGAC	ATATCGGTCA
14651	CTTCAGCAGC	CACCACAGAT	ATAGAGACAA	CGCATCCTTC	CATAAACACA
14701	GTAGTTACCA	ATGTGGGGAC	CACCGGTTCA	GCATTTGAAT	CACATTCTAC
14751	TGTCTCAGCT	TACCCAGAGC	CATCTAAAGT	CACATCTCCA	AATGTTACCA
14801	CCTCCACCAT	GGAAGACACC	ACAATTTCCT	GATCAATACC	TAAATCCTCT
14851	AAGACTACAA	GAACTGAGAC	TGAGACAAC	TCCTCCCTGA	CTCCTAAACT
14901	GAGGGAGACC	AGCATCTCCC	AGGAGATCAC	CTCGTCCACA	GAGACAAGCA
14951	CTGTTCCCTTA	CAAAGAGCTC	ACTGGTGCCA	CTACCGAGGT	ATCCAGGACA

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
15001	GATGTCACTT	CCTCTAGCAG	TACATCCTTC	CCTGGCCCTG	ATCAGTCCAC
15051	AGTGTCACTA	GACATCTCCA	CAGAAACCAA	CACCAGGCTG	TCTACCTCCC
15101	CAATAATGAC	AGAATCTGCA	GAAATAACCA	TCACCACCCA	AACAGGTCCT
15151	CATGGGGCTA	CATCACAGGA	TACTTTTACC	ATGGACCCAT	CAAATACAAC
15201	CCCCCAGGCA	GGGATCCACT	CAGCTATGAC	TCATGGATTT	TCACAATTGG
15251	ATGTGACCAC	TCTTATGAGC	AGAATTCCAC	AGGATGTATC	ATGGACAAGT
15301	CCTCCCTCTG	TGGATAAAAC	CAGCTCCCCC	TCTTCCTTTC	TGTCCTCACC
15351	TGCAATGACC	ACACCTTCCC	TGATTTCTTC	TACCTTACCA	GAGGATAAGC
15401	TCTCCTCTCC	TATGACTTCA	CTTCTCACCT	CTGGCCTAGT	GAAGATTACA
15451	GACATATTAC	GTACACGCTT	GGAACCTGTG	ACCAGCTCAC	TTCCAAATTT
15501	CAGCAGCACC	TCAGATAAGA	TACTGGCCAC	TTCTAAAGAC	AGTAAAGACA
15551	CAAAGGAAAT	TTTTCTTCT	ATAAACACAG	AAGAGACCAA	TGTGAAAGCC
15601	AACAACCTCTG	GACATGAATC	CCATTCCCCT	GCACTGGCTG	ACTCAGAGAC
15651	ACCCAAAGCC	ACAAC TCAA	TGGTTATCAC	CACCACTGTG	GGAGATCCAG
15701	CTCCTTCCAC	ATCAATGCCA	GTGCATGGTT	CCTCTGAGAC	TACAAACATT
15751	AAGAGAGAGC	CAACATATTT	CTTGACTCCT	AGACTGAGAG	AGACCAGTAC
15801	CTCTCAGGAG	TCCAGCTTTC	CCACGGACAC	AAGTTTCTA	CTTTCCAAAG
15851	TCCCCACTGG	TACTATTACT	GAGGTCTCCA	GTACAGGGGT	CAACTCTTCT
15901	AGCAAATTT	CCACCCCAGA	CCATGATAAG	TCCACAGTGC	CACCTGACAC
15951	CTTCACAGGA	GAGATCCCCA	GGGTCTTCAC	CTCCTCTATT	AAGACAAAT
16001	CTGCAGAAAT	GACGATCACC	ACCCAAGCAA	GTCCTCCTGA	GTCTGCATCG
16051	CACAGTACCC	TTCCCTTGGA	CACATCAACC	ACACTTTCCC	AGGGAGGGAC
16101	TCATTCAACT	GTGACTCAGG	GATTCCCATA	CTCAGAGGTG	ACCACTCTCA
16151	TGGGCATGGG	TCCTGGGAAT	GTGTCATGGA	TGACAACTCC	CCCTGTGGAA
16201	GAAACCAGCT	CTGTGTCTTC	CCTGATGTCT	TCACCTGCCA	TGACATCCCC

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
16251	TTCTCCTGTT	TCCTCCACAT	CACCACAGAG	CATCCCCTCC	TCTCCTCTTC
16301	CTGTGACTGC	ACTTCCTACT	TCTGTTCTGG	TGACAACCAC	AGATGTGTTG
16351	GGCACAACAA	GCCCAGAGTC	TGTAACCAGT	TCACCTCCAA	ATTGAGCAG
16401	CATCACTCAT	GAGAGACCGG	CCACTTACAA	AGACACTGCA	CACACAGAAG
16451	CCGCCATGCA	TCATTCCACA	AACACCGCAG	TGACCAATGT	AGGGACTTCC
16501	GGGTCTGGAC	ATAAATCACA	ATCCTCTGTC	CTAGCTGACT	CAGAGACATC
16551	GAAAGCCACA	CCTCTGATGA	GTACCACCTC	CACCCTGGGG	GACACAAGTG
16601	TTTCCACATC	AACTCCTAAT	ATCTCTCAGA	CTAACCAAAT	TCAAACAGAG
16651	CCAACAGCAT	CCCTGAGCCC	TAGACTGAGG	GAGAGCAGCA	CGTCTGAGAA
16701	GACCAGCTCA	ACAACAGAGA	CAAATACTGC	CTTTTCTTAT	GTGCCACAG
16751	GTGCTATTAC	TCAGGCCTCC	AGAACAGAAA	TCTCCTCTAG	CAGAACATCC
16801	ATCTCAGACC	TTGATCGGCC	CACAATAGCA	CCCGACATCT	CCACAGGAAT
16851	GATCACCAGG	CTCTTCACCT	CCCCCATCAT	GACAAAATCT	GCAGAAATGA
16901	CCGTCACCAC	TCAAACAAC	ACTCCTGGGG	CTACATCACA	GGGTATCCTT
16951	CCTTGGGACA	CATCAACCAC	ACTTTTCCAG	GGAGGGACTC	ATTCAACCGT
17001	GTCTCAGGGA	TTCCCACACT	CAGAGATAAC	CACTCTTCGG	AGCAGAACCC
17051	CTGGAGATGT	GTCATGGATG	ACAACTCCCC	CTGTGGAAGA	AACCAGCTCT
17101	GGGTTTCCC	TGATGTCACC	TTCCATGACA	TCCCCTTCTC	CTGTTTCCTC
17151	CACATCACCA	GAGAGCATCC	CCTCCTCTCC	TCTCCCTGTG	ACTGCACTTC
17201	TTACTTCTGT	TCTGGTGACA	ACCACCAATG	TATTGGGCAC	AACAAGCCCA
17251	GAGACCGTAA	CGAGTTCACC	TCCAAATTTA	AGCAGCCCCA	CACAGGAGAG
17301	ACTGACCACT	TACAAAGACA	CTGCGCACAC	AGAAGCCATG	CATGCTTCCA
17351	TGCATACAAA	CACTGCAGTG	GCCAACGTCG	GGACCTCCAT	TTCTGGACAT
17401	GAATCACAAT	CTTCTGTCCC	AGCTGATTCA	CACACATCCA	AAGCCACATC
17451	TCCAATGGGT	ATCACCTTCG	CCATGGGGGA	TACAAGTGTT	TCTACATCAA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

17501	CTCCTGCCTT	CTTTGAGACT	AGAATTCAGA	CTGAATCAAC	ATCCTCTTTG
17551	ATTCTTGGAT	TAAGGGACAC	CAGGACGTCT	GAGGAGATCA	AACTGTGAC
17601	AGAGACCAGC	ACTGTCCTTT	CAGAAGTGCC	CACTACTACT	ACTACTGAGG
17651	TCTCCAGGAC	AGAAGTTATC	ACTTCCAGCA	GAACAACCAT	CTCAGGGCCT
17701	GATCATTTCCA	AAATGTCACC	CTACATCTCC	ACAGAAACCA	TCACCAGGCT
17751	CTCCACTTTT	CCTTTTGTA	CAGGATCCAC	AGAAATGGCC	ATCACCAACC
17801	AAACAGGTCC	TATAGGGACT	ATCTCACAGG	CTACCCTTAC	CCTGGACACA
17851	TCAAGCACAG	CTTCCTGGGA	AGGGACTCAC	TCACCTGTGA	CTCAGAGATT
17901	TCCACACTCA	GAGGAGACCA	CTACTATGAG	CAGAAGTACT	AAGGGCGTGT
17951	CATGGCAAAG	CCCTCCCTCT	GTGGAAGAAA	CCAGTTCTCC	TTCTTCCCCA
18001	GTGCCTTTAC	CTGCAATAAC	CTCACATTCA	TCTCTTTATT	CCGCAGTATC
18051	AGGAAGTAGC	CCCCTTCTG	CTCTCCCTGT	GACTTCCCTT	CTCACCTCTG
18101	GCAGGAGGAA	GACCATAGAC	ATGTTGGACA	CACACTCAGA	ACTTGTGACC
18151	AGCTCCTTAC	CAAGTGCAAG	TAGCTTCTCA	GGTGAGATAC	TCATTCTGA
18201	AGCCTCCACA	AATACAGAGA	CAATTCACCT	TTCAGAGAAC	ACAGCAGAAA
18251	CCAATATGGG	GACCACCAAT	TCTATGCATA	AACTACATTC	CTCTGTCTCA
18301	ATCCACTCCC	AGCCATCCGG	ACACACACCT	CAAAGGTTA	CTGGATCTAT
18351	GATGGAGGAC	GCTATTGTTT	CCACATCAAC	ACCTGGTTCT	CCTGAGACTA
18401	AAAATGTTGA	CAGAGACTCA	ACATCCCCTC	TGACTCCTGA	ACTGAAAGAG
18451	GACAGCACCG	CCCTGGTGAT	GAACTCAACT	ACAGAGTCAA	AACTGTTTT
18501	CTCCAGTGTG	TCCCTGGATG	CTGCTACTGA	GGTCTCCAGG	GCAGAAGTCA
18551	CCTACTATGA	TCCTACATTC	ATGCCAGCTT	CTGCTCAGTC	AACAAAGTCC
18601	CCAGACATTT	CACCTGAAGC	CAGCAGCAGT	CATTCTAACT	CTCCTCCCTT
18651	GACAATATCT	ACACACAAGA	CCATCGCCAC	ACAAACAGGT	CCTTCTGGGG
18701	TGACATCTCT	TGGCCAACTG	ACCCTGGACA	CATCAACCAT	AGCCACCTCA

Table 4 (continued)

Human cDNA of CA125 (SEQ ID NO: 4)					
18751	GCAGGAACTC	CATCAGCCAG	AACTCAGGAT	TTTGTAGATT	CAGAAACAAC
18801	CAGTGTCATG	AACAATGATC	TCAATGATGT	GTTGAAGACA	AGCCCTTTCT
18851	CTGCAGAAGA	AGCCAACTCT	CTCTCTTCTC	AGGCACCTCT	CCTTGTGACA
18901	ACCTCACCTT	CTCCTGTAAC	TTCCACATTG	CAAGAGCACA	GTACCTCCTC
18951	TCTTGTTTCT	GTGACCTCAG	TACCCACCCC	TACACTGGCG	AAGATCACAG
19001	ACATGGACAC	AAACTTAGAA	CCTGTGACTC	GTTACCTCA	AAATTTAAGG
19051	AACACCTTGG	CCACTTCAGA	AGCCACCACA	GATACACACA	CAATGCATCC
19101	TTCTATAAAC	ACAGCAATGG	CCAATGTGGG	GACCACCAGT	TCACCAAATG
19151	AATTCTATTT	TACTGTCTCA	CCTGACTCAG	ACCCATATAA	AGCCACATCC
19201	GCAGTAGTTA	TCACTTCCAC	CTCGGGGGAC	TCAATAGTTT	CCACATCAAT
19251	GCCTAGATCC	TCTGCGATGA	AAAAGATTGA	GTCTGAGACA	ACTTTCTCCC
19301	TGATATTTAG	ACTGAGGGAG	ACTAGCACCT	CCCAGAAAAT	TGGCTCATCC
19351	TCAGACACAA	GCACGGTCTT	TGACAAAGCA	TTCCTGCTG	CTACTACTGA
19401	GGTCTCCAGA	ACAGAACTCA	CCTCCTCTAG	CAGAACATCC	ATCCAAGGCA
19451	CTGAAAAGCC	CACAATGTCA	CCGGACACCT	CCACAAGATC	TGTCACCATG
19501	CTTTCTACTT	TTGCTGGCCT	GACAAAATCC	GAAGAAAGGA	CCATTGCCAC
19551	CCAAACAGGT	CCTCATAGGG	CGACATCACA	GGGTACCCTT	ACCTGGGACA
19601	CATCAATCAC	AACCTCACAG	GCAGGGACCC	ACTCAGCTAT	GACTCATGGA
19651	TTTTCACAAT	TAGATTTGTC	CACTCTTACG	AGTAGAGTTC	CTGAGTACAT
19701	ATCAGGGACA	AGCCCACCCT	CTGTGGAAAA	AACCAGCTCT	TCCTCTTCCC
19751	TTCTGTCTTT	ACCAGCAATA	ACCTCACCGT	CCCCTGTACC	TACTACATTA
19801	CCAGAAAGTA	GGCCGTCTTC	TCCTGTTCAT	CTGACTTCAC	TCCCCACCTC
19851	TGGCCTAGTG	AAGACCACAG	ATATGCTGGC	ATCTGTGGCC	AGTTTACCTC
19901	CAAACCTGGG	CAGCACCTCA	CATAAGATAC	CGACTACTTC	AGAAGACATT
19951	AAAGATACAG	AGAAAATGTA	TCCTTCCACA	AACATAGCAG	TAACCAATGT

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

20001	GGGGACCACC	ACTTCTGAAA	AGGAATCTTA	TTCGTCTGTC	CCAGCCTACT
20051	CAGAACCACC	CAAAGTCACC	TCTCCAATGG	TTACCTCTTT	CAACATAAGG
20101	GACACCATTG	TTCCACATC	CATGCCTGGC	TCCTCTGAGA	TTACAAGGAT
20151	TGAGATGGAG	TCAACATTCT	CCGTGGCTCA	TGGGCTGAAG	GGAACCAGCA
20201	CCTCCCAGGA	CCCCATCGTA	TCCACAGAGA	AAAGTGCTGT	CCTTCACAAG
20251	TTGACCACTG	GTGCTACTGA	GACCTCTAGG	ACAGAAGTTG	CCTCTTCTAG
20301	AAGAACATCC	ATTCCAGGCC	CTGATCATTC	CACAGAGTCA	CCAGACATCT
20351	CCACTGAAGT	GATCCCCAGC	CTGCCTATCT	CCCTTGGCAT	TACAGAATCT
20401	TCAAATATGA	CCATCATCAC	TCGAACAGGT	CCTCCTCTTG	GCTCTACATC
20451	ACAGGGCACA	TTTACCTTGG	ACACACCAAC	TACATCCTCC	AGGGCAGGAA
20501	CACACTCGAT	GGCGACTCAG	GAATTTCCAC	ACTCAGAAAT	GACCACTGTC
20551	ATGAACAAGG	ACCCTGAGAT	TCTATCATGG	ACAATCCCTC	CTTCTATAGA
20601	GAAAACCAGC	TTCTCCTCTT	CCCTGATGCC	TTCACCAGCC	ATGACTTCAC
20651	CTCCTGTTTC	CTCAACATTA	CCAAAGACCA	TTACACCCAC	TCCTTCTCCT
20701	ATGACCTCAC	TGCTCACCCC	TAGCCTAGTG	ATGACCACAG	ACACATTGGG
20751	CACAAGCCCA	GAACCTACAA	CCAGTTCACC	TCCAAATTTG	AGCAGTACCT
20801	CACATGTGAT	ACTGACAACA	GATGAAGACA	CCACAGCTAT	AGAAGCCATG
20851	CATCCTTCCA	CAAGCACAGC	AGCGACTAAT	GTGGAAACCA	CCTGTTCTGG
20901	ACATGGGTCA	CAATCCTCTG	TCCTAACTGA	CTCAGAAAAA	ACCAAGGCCA
20951	CAGCTCCAAT	GGATACCACC	TCCACCATGG	GGCATACAAC	TGTTTCCACA
21001	TCAATGTCTG	TTTCCTCTGA	GACTACAAAA	ATTAAGAGAG	AGTCAACATA
21051	TTCTTGA	CCTGGACTGA	GAGAGACCAG	CATTTCCCAA	AATGCCAGCT
21101	TTTCCACTGA	CACAAGTATT	GTTCTTTCAG	AAGTCCCCAC	TGGTACTACT
21151	GCTGAGGTCT	CCAGGACAGA	AGTCACCTCC	TCTGGTAGAA	CATCCATCCC
21201	TGGCCCTTCT	CAGTCCACAG	TTTTGCCAGA	AATATCCACA	AGAACAATGA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

21251	CAAGGCTCTT	TGCCTCGCCC	ACCATGACAG	AATCAGCAGA	AATGACCATC
21301	CCCACTCAAA	CAGGTCCTTC	TGGGTCTACC	TCACAGGATA	CCCTTACCTT
21351	GGACACATCC	ACCACAAAGT	CCCAGGCAAA	GACTCATTCA	ACTTTGACTC
21401	AGAGATTTCC	ACACTCAGAG	ATGACCACTC	TCATGAGCAG	AGGTCTTGGA
21451	GATATGTCAT	GGCAAAGCTC	TCCCTCTCTG	GAAAATCCCA	GCTCTCTCCC
21501	TTCCCTGCTG	TCTTTACCTG	CCACAACCTC	ACCTCCTCCC	ATTTCTCCA
21551	CATTACCAGT	GACTATCTCC	TCCTCTCCTC	TTCCTGTGAC	TTCATTCTC
21601	ACCTCTAGCC	CGGTAACGAC	CACAGACATG	TTACACACAA	GCCCAGAACT
21651	TGTAACCAGT	TCACCTCCAA	AGCTGAGCCA	CAC TTCAGAT	GAGAGACTGA
21701	CCACTGGCAA	GGACACCACA	AATACAGAAG	CTGTGCATCC	TTCCACAAAC
21751	ACAGCAGCGT	CCAATGTGGA	GATTCCCAGC	TTTGGACATG	AATCCCCTTC
21801	CTCTGCCTTA	GCTGACTCAG	AGACATCCAA	AGCCACATCA	CCAATGTTTA
21851	TTACCTCCAC	CCAGGAGGAT	ACAACTGTTG	CCATATCAAC	CCCTCACTTC
21901	TTGGAGACTA	GCAGAATTCA	GAAAGAGTCA	ATTCCTCCC	TGAGCCCTAA
21951	ATTGAGGGAG	ACAGGCAGTT	CTGTGGAGAC	AAGCTCAGCC	ATAGAGACAA
22001	GTGCTGTCCT	TTCTGAAGTG	TCCATTGGTG	CTACTACTGA	GATCTCCAGG
22051	ACAGAAGTCA	CCTCCTCTAG	CAGAACATCC	ATCTCTGGTT	CTGCTGAGTC
22101	CACAATGTTG	CCAGAAATAT	CCACCACAAG	AAAAATCATT	AAGTTCCCTA
22151	CTTCCCCCAT	CCTGGCAGAA	TCATCAGAAA	TGACCATCAA	GACCCAAACA
22201	AGTCCTCCTG	GGTCTACATC	AGAGAGTACC	TTTACATTAG	ACACATCAAC
22251	CACTCCCTCC	TTGGTAATAA	CCCATTCGAC	TATGACTCAG	AGATTGCCAC
22301	ACTCAGAGAT	AACCACTCTT	GTGAGTAGAG	GTGCTGGGGA	TGTGCCACGG
22351	CCCAGCTCTC	TCCCTGTGGA	AGAAACAAGC	CCTCCATCTT	CCCAGCTGTC
22401	TTTATCTGCC	ATGATCTCAC	CTTCTCCTGT	TTCTTCCACA	TTACCAGCAA
22451	GTAGCCACTC	CTCTTCTGCT	TCTGTGACTT	CACCTCTCAC	ACCAGGCCAA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

22501	GTGAAGACTA	CTGAGGTGTT	GGACGCAAGT	GCAGAACCTG	AAACCAGTTC
22551	ACCTCCAAGT	TTGAGCAGCA	CCTCAGTTGA	AATACTGGCC	ACCTCTGAAG
22601	TCACCACAGA	TACGGAGAAA	ATTCATCCTT	TCCCAAACAC	GGCAGTAACC
22651	AAAGTTGGAA	CTTCCAGTTC	TGGACATGAA	TCCCCTTCCT	CTGTCCTACC
22701	TGACTCAGAG	ACAACCAAAG	CCACATCGGC	AATGGGTACC	ATCTCCATTA
22751	TGGGGGATAC	AAGTGTTTCT	ACATTAACTC	CTGCCTTATC	TAACACTAGG
22801	AAAATTTCAGT	CAGAGCCAGC	TTCCTCACTG	ACCACCAGAT	TGAGGGAGAC
22851	CAGCACCTCT	GAAGAGACCA	GCTTAGCCAC	AGAAGCAAAC	ACTGTTCTTT
22901	CTAAAGTGTC	CACTGGTGCT	ACTACTGAGG	TCTCCAGGAC	AGAAGCCATC
22951	TCCTTTAGCA	GAACATCCAT	GTCAGGCCCT	GAGCAGTCCA	CAATGTCACA
23001	AGACATCTCC	ATAGGAACCA	TCCCCAGGAT	TTCTGCCTCC	TCTGTCCTGA
23051	CAGAATCTGC	AAAAATGACC	ATCACAACCC	AAACAGGTCC	TTCGGAGTCT
23101	ACACTAGAAA	GTACCCCTTA	TTTGAACACA	GCAACCACAC	CCTCTTGGGT
23151	GGAAACCCAC	TCTATAGTAA	TTCAGGGATT	TCCACACCCA	GAGATGACCA
23201	CTTCCATGGG	CAGAGGTCCT	GGAGGTGTGT	CATGGCCTAG	CCCTCCCTTT
23251	GTGAAAGAAA	CCAGCCCTCC	ATCCTCCCCG	CTGTCTTTAC	CTGCCGTGAC
23301	CTCACCTCAT	CCTGTTTCCA	CCACATTCT	AGCACATATC	CCCCCTCTC
23351	CCCTTCCTGT	GACTTCACTT	CTCACCTCTG	GCCCGGCGAC	AACCACAGAT
23401	ATCTTGGGTA	CAAGCACAGA	ACCTGGAACC	AGTTCATCTT	CAAGTTTGAG
23451	CACCACCTCC	CATGAGAGAC	TGACCACTTA	CAAAGACACT	GCACATACAG
23501	AAGCCGTGCA	TCCTTCCACA	AACACAGGAG	GGACCAATGT	GGCAACCACC
23551	AGCTCTGGAT	ATAAATCACA	GTCCTCTGTC	CTAGCTGACT	CATCTCCAAT
23601	GTGTACCACC	TCCACCATGG	GGGATACAAG	TGTTCTCACA	TCAACTCCTG
23651	CCTTCCTTGA	GACTAGGAGG	ATTCAGACAG	AGCTAGCTTC	CTCCCTGACC
23701	CCTGGATTGA	GGGAGTCCAG	TGGCTCTGAA	GGGACCAGCT	CAGGCACCAA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

23751	GATGAGCACT	GTCCTCTCTA	AAGTGCCAC	TGGTGCTACT	ACTGAGATCT
23801	CCAAGGAAGA	CGTCACCTCC	ATCCCAGGTC	CCGCTCAATC	CACAATATCA
23851	CCAGACATCT	CCACAAGAAC	CGTCAGCTGG	TTCTCTACAT	CCCCTGTCAT
23901	GACAGAATCA	GCAGAAATAA	CCATGAACAC	CCATACAAGT	CCTTTAGGGG
23951	CCACAACACA	AGGCACCAGT	ACTTTGGCCA	CGTCAAGCAC	AACCTCTTTG
24001	ACAATGACAC	ACTCAACTAT	ATCTCAAGGA	TTTTCACACT	CACAGATGAG
24051	CACTCTTATG	AGGAGGGGTC	CTGAGGATGT	ATCATGGATG	AGCCCTCCCC
24101	TTCTGGAAAA	AACTAGACCT	TCCTTTTCTC	TGATGTCTTC	ACCAGCCACA
24151	ACTTCACCTT	CTCCTGTTTC	CTCCACATTA	CCAGAGAGCA	TCTCTTCCTC
24201	TCCTCTTCCT	GTGACTTCAC	TCCTCACGTC	TGGCTTGGCA	AAACTACAG
24251	ATATGTTGCA	CAAAAGCTCA	GAACCTGTAA	CCAACTCACC	TGCAAATTTG
24301	AGCAGCACCT	CAGTTGAAAT	ACTGGCCACC	TCTGAAGTCA	CCACAGATAC
24351	AGAGAAAAC	CATCCTTCTT	CAAACAGAAC	AGTGACCGAT	GTGGGGACCT
24401	CCAGTTCTGG	ACATGAATCC	ACTTCCTTTG	TCCTAGCTGA	CTCACAGACA
24451	TCCAAAGTCA	CATCTCCAAT	GGTTATTACC	TCCACCATGG	AGGATACGAG
24501	TGTCTCCACA	TCAACTCCTG	GCTTTTTTGA	GACTAGCAGA	ATTCAGACAG
24551	AACCAACATC	CTCCCTGACC	CTTGGACTGA	GAAAGACCAG	CAGCTCTGAG
24601	GGGACCAGCT	TAGCCACAGA	GATGAGCACT	GTCCTTTCTG	GAGTGCCAC
24651	TGGTGCCACT	GCTGAAGTCT	CCAGGACAGA	AGTCACCTCC	TCTAGCAGAA
24701	CATCCATCTC	AGGCTTTGCT	CAGCTCACAG	TGTCACCAGA	GACTTCCACA
24751	GAAACCATCA	CCAGACTCCC	TACCTCCAGC	ATAATGACAG	AATCAGCAGA
24801	AATGATGATC	AAGACACAAA	CAGATCCTCC	TGGGTCTACA	CCAGAGAGTA
24851	CTCATACTGT	GGACATATCA	ACAACACCCA	ACTGGGTAGA	AACCCACTCG
24901	ACTGTGACTC	AGAGATTTTC	AACTCAGAG	ATGACCACTC	TTGTGAGCAG
24951	AAGCCCTGGT	GATATGTTAT	GGCCTAGTCA	ATCCTCTGTG	GAAGAAACCA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

25001	GCTCTGCCTC	TCCCTGCTG	TCTCTGCCTG	CCACGACCTC	ACCTTCTCCT
25051	GTTTCCTCTA	CATTAGTAGA	GGATTTCCCT	TCCGCTTCTC	TTCCTGTGAC
25101	TTCTCTTCTC	ACCCCTGGCC	TGGTGATAAC	CACAGACAGG	ATGGGCATAA
25151	GCAGAGAACC	TGGAACCAGT	TCCACTTCAA	ATTTGAGCAG	CACCTCCCAT
25201	GAGAGACTGA	CCACTTTGGA	AGACACTGTA	GATACAGAAG	ACATGCAGCC
25251	TTCCACACAC	ACAGCAGTGA	CCAACGTGAG	GACCTCCATT	TCTGGACATG
25301	AATCACAATC	TTCTGTCCTA	TCTGACTCAG	AGACACCCAA	AGCCACATCT
25351	CCAATGGGTA	CCACCTACAC	CATGGGGGAA	ACGAGTGTTT	CCATATCCAC
25401	TTCTGACTTC	TTTGAGACCA	GCAGAATTCA	GATAGAACCA	ACATCCTCCC
25451	TGACTTCTGG	ATTGAGGGAG	ACCAGCAGCT	CTGAGAGGAT	CAGCTCAGCC
25501	ACAGAGGGAA	GCACTGTCCT	TTCTGAAGTG	CCCAGTGGTG	CTACCACTGA
25551	GGTCTCCAGG	ACAGAAGTGA	TATCCTCTAG	GGGAACATCC	ATGTCAGGGC
25601	CTGATCAGTT	CACCATATCA	CCAGACATCT	CTACTGAAGC	GATCACCAGG
25651	CTTTCTACTT	CCCCATTAT	GACAGAATCA	GCAGAAAGTG	CCATCACTAT
25701	TGAGACAGGT	TCTCCTGGGG	CTACATCAGA	GGGTACCCTC	ACCTTGGACA
25751	CCTCAACAAC	AACCTTTTGG	TCAGGGACCC	ACTCAACTGC	ATCTCCAGGA
25801	TTTTCACACT	CAGAGATGAC	CACTCTTATG	AGTAGAACTC	CTGGAGATGT
25851	GCCATGGCCG	AGCCTTCCCT	CTGTGGAAGA	AGCCAGCTCT	GTCTCTTCCT
25901	CACTGTCTTC	ACCTGCCATG	ACCTCAACTT	CTTTTTTCTC	CGCATTACCA
25951	GAGAGCATCT	CCTCCTCTCC	TCATCCTGTG	ACTGCACTTC	TCACCCTTGG
26001	CCCAGTGAAG	ACCACAGACA	TGTTGCGCAC	AAGCTCAGAA	CCTGAAACCA
26051	GTTACCTCC	AAATTTGAGC	AGCACCTCAG	CTGAAATATT	AGCCACGTCT
26101	GAAGTCACCA	AAGATAGAGA	GAAAATTCAT	CCCTCCTCAA	ACACACCTGT
26151	AGTCAATGTA	GGGACTGTGA	TTTATAAACA	TCTATCCCCT	TCCTCTGTTT
26201	TGGCTGACTT	AGTGACAACA	AAACCCACAT	CTCCAATGGC	TACCACCTCC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

26251	ACTCTGGGGA	ATACAAGTGT	TTCCACATCA	ACTCCTGCCT	TCCCAGAAAC
26301	TATGATGACA	CAGCCAACTT	CCTCCCTGAC	TTCTGGATTA	AGGGAGATCA
26351	GTACCTCTCA	AGAGACCAGC	TCAGCAACAG	AGAGAAGTGC	TTCTCTTTCT
26401	GGAATGCCCA	CTGGTGCTAC	TACTAAGGTC	TCCAGAACAG	AAGCCCTCTC
26451	CTTAGGCAGA	ACATCCACCC	CAGGTCCTGC	TCAATCCACA	ATATCACCAG
26501	AAATCTCCAC	GGAAACCATC	ACTAGAATTT	CTACTCCCCT	CACCACGACA
26551	GGATCAGCAG	AAATGACCAT	CACCCCCAAA	ACAGGTCATT	CTGGGGCATC
26601	CTCACAAGGT	ACCTTTACCT	TGGACACATC	AAGCAGAGCC	TCCTGGCCAG
26651	GAACTCACTC	AGCTGCAACT	CACAGATCTC	CACACTCAGG	GATGACCACT
26701	CCTATGAGCA	GAGGTCCTGA	GGATGTGTCA	TGGCCAAGCC	GCCCATCAGT
26751	GGAAAAAACT	AGCCCTCCAT	CTTCCCTGGT	GTCTTTATCT	GCAGTAACCT
26801	CACCTTCGCC	ACTTTATTCC	ACACCATCTG	AGAGTAGCCA	CTCATCTCCT
26851	CTCCGGGTGA	CTTCTCTTTT	CACCCCTGTC	ATGATGAAGA	CCACAGACAT
26901	GTTGGACACA	AGCTTGGAAC	CTGTGACCAC	TTACCTCCC	AGTATGAATA
26951	TCACCTCAGA	TGAGAGTCTG	GCCACTTCTA	AAGCCACCAT	GGAGACAGAG
27001	GCAATTCAGC	TTTCAGAAAA	CACAGCTGTG	ACTCAGATGG	GCACCATCAG
27051	CGCTAGACAA	GAATTCTATT	CCTCTTATCC	AGGCCTCCCA	GAGCCATCCA
27101	AAGTGACATC	TCCAGTGGTC	ACCTCTTCCA	CCATAAAAGA	CATTGTTTCT
27151	ACAACCATAC	CTGCTTCCTC	TGAGATAACA	AGAATTGAGA	TGGAGTCAAC
27201	ATCCACCCTG	ACCCCCACAC	CAAGGGAGAC	CAGCACCTCC	CAGGAGATCC
27251	ACTCAGCCAC	AAAGCCAAGC	ACTGTTTCCTT	ACAAGGCACT	CACTAGTGCC
27301	ACGATTGAGG	ACTCCATGAC	ACAAGTCATG	TCCTCTAGCA	GAGGACCTAG
27351	CCCTGATCAG	TCCACAATGT	CACAAGACAT	ATCCAGTGAA	GTGATCACCA
27401	GGCTCTCTAC	CTCCCCCATC	AAGGCAGAAT	CTACAGAAAT	GACCATTACC
27451	ACCCAAACAG	GTTCTCCTGG	GGCTACATCA	AGGGGTACCC	TTACCTTGGA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

27501	CACTTCAACA	ACTTTTATGT	CAGGGACCCA	CTCAACTGCA	TCTCAAGGAT
27551	TTTCACACTC	ACAGATGACC	GCTCTTATGA	GTAGAACTCC	TGGAGATGTG
27601	CCATGGCTAA	GCCATCCCTC	TGTGGAAGAA	GCCAGCTCTG	CCTCTTTCTC
27651	ACTGTCTTCA	CCTGTCATGA	CCTCATCTTC	TCCCGTTTCT	TCCACATTAC
27701	CAGACAGCAT	CCACTCTTCT	TCGCTTCCTG	TGACATCACT	TCTCACCTCA
27751	GGGCTGGTGA	AGACCACAGA	GCTGTTGGGC	ACAAGCTCAG	AACCTGAAAC
27801	CAGTTCACCC	CCAAATTTGA	GCAGCACCTC	AGCTGAAATA	CTGGCCACCA
27851	CTGAAGTCAC	TACAGATACA	GAGAACTGG	AGATGACCAA	TGTGGTAACC
27901	TCAGGTTATA	CACATGAATC	TCCTTCCTCT	GTCCTAGCTG	ACTCAGTGAC
27951	AACAAAGGCC	ACATCTTCAA	TGGGTATCAC	CTACCCACACA	GGAGATACAA
28001	ATGTTCTCAC	ATCAACCCCT	GCCTTCTCTG	ACACCAGTAG	GATTCAAACA
28051	AAGTCAAAGC	TCTCACTGAC	TCCTGGGTTG	ATGGAGACCA	GCATCTCTGA
28101	AGAGACCAGC	TCTGCCACAG	AAAAAAGCAC	TGTCCTTTCT	AGTGTGCCCCA
28151	CTGGTGCTAC	TACTGAGGTC	TCCAGGACAG	AAGCCATCTC	TTCTAGCAGA
28201	ACATCCATCC	CAGGCCCTGC	TCAATCCACA	ATGTCATCAG	ACACCTCCAT
28251	GGAAACCATC	ACTAGAATTT	CTACCCCCCT	CACAAGGAAA	GAATCAACAG
28301	ACATGGCCAT	CACCCCCAAA	ACAGGTCCTT	CTGGGGCTAC	CTCGCAGGGT
28351	ACCTTTACCT	TGGACTCATC	AAGCACAGCC	TCCTGGCCAG	GAATCACTC
28401	AGCTACAACT	CAGAGATTTT	CACAGTCAGT	GGTGACAACT	CCTATGAGCA
28451	GAGGTCTCTGA	GGATGTGTCA	TGGCCAAGCC	CGCTGTCTGT	GGAAAAAACC
28501	AGCCCTCCAT	CTTCCCTGGT	ATCTTCATCT	TCAGTAACCT	CACCTTCGCC
28551	ACTTTATTCC	ACACCATCTG	GGAGTAGCCA	CTCCTCTCCT	GTCCCTGTCA
28601	CTTCTCTTTT	EACCTCTATC	ATGATGAAGG	CCACAGACAT	GTTGGATGCA
28651	AGTTTGGAAC	CTGAGACCAC	TTCAGCTCCC	AATATGAATA	TCACCTCAGA
28701	TGAGAGTCTG	GCCACTTCTA	AAGCCACCAC	GGAGACAGAG	GCAATTCACG

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

28751	TTTTTGAAAA	TACAGCAGCG	TCCCATGTGG	AAACCACCAG	TGCTACAGAG
28801	GAAGTCTATT	CCTCTTCCCC	AGGCTTCTCA	GAGCCAACAA	AAGTGATATC
28851	TCCAGTGGTC	ACCTCTTCCT	CTATAAGAGA	CAACATGGTT	TCCACAACAA
28901	TGCCTGGCTC	CTCTGGCATT	ACAAGGATTG	AGATAGAGTC	AATGTCATCT
28951	CTGACCCCTG	GACTGAGGGA	GACCAGAACC	TCCCAGGACA	TCACCTCATC
29001	CACAGAGACA	AGCACTGTCC	TTTACAAGAT	GTCCTCTGGT	GCCACTCCTG
29051	AGGTCTCCAG	GACAGAAGTT	ATGCCCTCTA	GCAGAACATC	CATTCTGGC
29101	CCTGCTCAGT	CCACAATGTC	ACTAGACATC	TCCGATGAAG	TTGTCACCAG
29151	GCTGTCTACC	TCTCCCATCA	TGACAGAATC	TGCAGAAATA	ACCATCACCA
29201	CCCAAACAGG	TTATTCTCTG	GCTACATCCC	AGGTTACCCT	TCCCTTGGGC
29251	ACCTCAATGA	CCTTTTTGTC	AGGGACCCAC	TCAACTATGT	CTCAAGGACT
29301	TTCACTCA	GAGATGACCA	ATCTTATGAG	CAGGGGTCTT	GAAAGTCTGT
29351	CATGGACGAG	CCCTCGCTTT	GTGGAAACAA	CTAGATCTTC	CTCTTCTCTG
29401	ACATCATTAC	CTCTCACGAC	CTCACTTTCT	CCTGTGTCCT	CCACATTACT
29451	AGACAGTAGC	CCCTCCTCTC	CTCTTCCTGT	GAATTCACTT	ATCCTCCCAG
29501	GCCTGGTGAA	GACTACAGAA	GTGTTGGATA	CAAGCTCAGA	GCCTAAAACC
29551	AGTTCATCTC	CAAATTTGAG	CAGCACCTCA	GTTGAAATAC	CGGCCACCTC
29601	TGAAATCATG	ACAGATACAG	AGAAAATTCA	TCCTTCTCTA	AACACAGCGG
29651	TGGCCAAAGT	GAGGACCTCC	AGTTCTGTTC	ATGAATCTCA	TTCTCTGTC
29701	CTAGCTGACT	CAGAAACAAC	CATAACCATA	CCTTCAATGG	GTATCACCTC
29751	CGCTGTGGAC	GATACCACTG	TTTTCACATC	AAATCCTGCC	TTCTCTGAGA
29801	CTAGGAGGAT	TCCGACAGAG	CCAACATTCT	CATTGACTCC	TGGATTGAGG
29851	GAGACTAGCA	CCTCTGAAGA	GACCACCTCA	ATCACAGAAA	CAAGTGCAGT
29901	CCTTTATGGA	GTGCCCATA	GTGCTACTAC	TGAAGTCTCC	ATGACAGAAA
29951	TCATGTCCTC	TAATAGAACA	CACATCCCTG	ACTCTGATCA	GTCCACGATG

Table 4 (continued)

 Human cDNA of CA125
 (SEQ ID NO: 4)

30001 TCTCCAGACA TCATCACTGA AGTGATCACC AGGCTCTCTT CCTCATCCAT
 30051 GATGTCAGAA TCAACACAAA TGACCATCAC CACCCAAAAA AGTTCTCCTG
 30101 GGGCTACAGC ACAGAGTACT CTTACCTTGG CCACAACAAC AGCCCCCTTG
 30151 GCAAGGACCC ACTCAACTGT TCCTCCTAGA TTTTACACT CAGAGATGAC
 30201 AACTCTTATG AGTAGGAGTC CTGAAAATCC ATCATGGAAG AGCTCTCCCT
 30251 TTGTGGAAAA AACTAGCTCT TCATCTTCTC TGTTGTCCTT ACCTGTCACG
 30301 ACCTCACCTT CTGTTTCTTC CACATTACCG CAGAGTATCC CTCCTCCTC
 30351 TTTTCTGTG ACTTCACTCC TCACCCAGG CATGGTGAAG ACTACAGACA
 30401 CAAGCACAGA ACCTGGAACC AGTTTATCTC CAAATCTGAG TGGCACCTCA
 30451 GTTGAAATAC TGGCTGCCTC TGAAGTCACC ACAGATACAG AGAAAATTCA
 30501 TCCTTCTTCA AGCATGGCAG TGACCAATGT GGAACCACC AGTTCTGGAC
 30551 ATGAACTATA TTCCTCTGTT TCAATCCACT CGGAGCCATC CAAGGCTACA
 30601 TACCCAGTGG GTACTCCCTC TTCCATGGCT GAAACCTCTA TTTCCACATC
 30651 AATGCCTGCT AATTTTGAGA CCACAGGATT TGAGGCTGAG CCATTTTCTC
 30701 ATTTGACTTC TGGATTTAGG AAGACAAACA TGTCCCTGGA CACCAGCTCA
 30751 GTCACACCAA CAAATACACC TTCTTCTCCT GGGTCCACTC ACCTTTTACA
 30801 GAGTTCCAAG ACTGATTTC CTTCTTCTGC AAAAACATCA TCCCCAGACT
 30851 GGCCTCCAGC CTCACAGTAT ACTGAAATTC CAGTGGACAT AATCACCCCC
 30901 TTTAATGCTT CTCCATCTAT TACGGAGTCC ACTGGGATAA CCTCCTTCCC
 30951 AGAATCCAGG TTTACTATGT CTGTAACAGA AAGTACTCAT CATCTGAGTA
 31001 CAGATTTGCT GCCTTCAGCT GAGACTATTT CCACTGGCAC AGTGATGCCT
 31051 TCTCTATCAG AGGCCATGAC TTCATTGACC ACCACTGGAG TTCCACGAGC
 31101 CATCTCAGGT- TCAGGTAGTC CATTCTCTAG GACAGAGTCA GGCCCTGGGG
 31151 ATGCTACTCT GTCCACCATT GCAGAGAGCC TGCCTTCATC CACTCCTGTG
 31201 CCATTCTCCT CTTCAACCTT CACTACCACT GATTCTTCAA CCATCCCAGC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

31251	CCTCCATGAG	ATAACTTCCT	CTTCAGCTAC	CCCATATAGA	GTGGACACCA
31301	GTCTTGGGAC	AGAGAGCAGC	ACTACTGAAG	GACGCTTGGT	TATGGTCAGT
31351	ACTTTGGACA	CTTCAAGCCA	ACCAGGCAGG	ACATCTTCAA	CACCCATTTT
31401	GGATACCAGA	ATGACAGAGA	GCGTTGAGCT	GGGAACAGTG	ACAAGTGCTT
31451	ATCAAGTTCC	TTCACCTCTCA	ACACGGTTGA	CAAGAACTGA	TGGCATTATG
31501	GAACACATCA	CAAAAATACC	CAATGAAGCA	GCACACAGAG	GTACCATAAG
31551	ACCAGTCAAA	GGCCCTCAGA	CATCCACTTC	GCCTGCCAGT	CCTAAAGGAC
31601	TACACACAGG	AGGGACAAAA	AGAATGGAGA	CCACCACCAC	AGCTTTGAAG
31651	ACCACCACCA	CAGCTTTGAA	GACCACTTCC	AGAGCCACCT	TGACCACCAG
31701	TGTCTATACT	CCCACTTTGG	GAACACTGAC	TCCCCTCAAT	GCATCAAGGC
31751	AAATGGCCAG	CACAATCCTC	ACAGAAATGA	TGATCACAAC	CCCATATGTT
31801	TTCCCTGATG	TTCCAGAAAC	GACATCCTCA	TTGGCTACCA	GCCTGGGAGC
31851	AGAAACCAGC	ACAGCTCTTC	CCAGGACAAC	CCCATCTGTT	CTCAATAGAG
31901	AATCAGAGAC	CACAGCCTCA	CTGGTCTCTC	GTTCTGGGGC	AGAGAGAAGT
31951	CCGGTTATTG	AAACTCTAGA	TGTTTCTTCT	AGTGAGCCAG	ATACAACAGC
32001	TTTCATGGGT	ATCCATCCTG	CAGAGACCAT	CCCAACTGTT	TCCAAGACAA
32051	CCCCCAATTT	TTTCCACAGT	GAATTAGACA	CTGTATCTTC	CACAGCCACC
32101	AGTCATGGGG	CAGACGTCAG	CTCAGCCATT	CCAACAAATA	TCTCACCTAG
32151	TGAACTAGAT	GCACTGACCC	CACTGGTCAC	TATTTTCGGG	ACAGATACTA
32201	GTACAACATT	CCCAACACTG	ACTAAGTCCC	CACATGAAAC	AGAGACAAGA
32251	ACCACATGGC	TCACTCATCC	TGCAGAGACC	AGCTCAACTA	TTCCCAGAAC
32301	AATCCCCAAT	TTTTCTCATC	ATGAATCAGA	TGCCACACCT	TCAATAGCCA
32351	CCAGTCCTGG	GGCAGAAACC	AGTTCAGCTA	TTCCAATTAT	GACTGTCTCA
32401	CCTGGTGCAG	AAGATCTGGT	GACCTCACAG	GTCAC TAGTT	CTGGGACAGA
32451	CAGAAATATG	ACTATTCCAA	CTTTGACTCT	TTCTCCTGGT	GAACCAAAGA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

32501	CGATAGCCTC	ATTAGTCACC	CATCCTGAAG	CACAGACAAG	TTCGGCCATT
32551	CCAACTTCAA	CTATCTCGCC	TGCTGTATCA	CGGTTGGTGA	CCTCAATGGT
32601	CACCAGTTTG	GCGGCAAAGA	CAAGTACAAC	TAATCGAGCT	CTGACAAACT
32651	CCCCTGGTGA	ACCAGCTACA	ACAGTTTCAT	TGGTCACGCA	TCCTGCACAG
32701	ACCAGCCCAA	CAGTTCCTTG	GACAACTTCC	ATTTTTTTTCC	ATAGTAAATC
32751	AGACACCACA	CCTTCAATGA	CCACCAGTCA	TGGGGCAGAA	TCCAGTTCAG
32801	CTGTTCCAAC	TCCAACGTGT	TCAACTGAGG	TACCAGGAGT	AGTGACCCCT
32851	TTGGTCACCA	GTTCTAGGGC	AGTGATCAGT	ACAACTATTTC	CAATTCTGAC
32901	TCTTTCTCCT	GGTGAACCAG	AGACCACACC	TTCAATGGCC	ACCAGTCATG
32951	GGGAAGAAGC	CAGTTCCTGCT	ATTCCAACCTC	CAACTGTTTC	ACCTGGGGTA
33001	CCAGGAGTGG	TGACCTCTCT	GGTCACTAGT	TCTAGGGCAG	TGACTAGTAC
33051	AACTATTCCA	ATTCTGACTT	TTTCTCTTGG	TGAACCAGAG	ACCACACCTT
33101	CAATGGCCAC	CAGTCATGGG	ACAGAAGCTG	GCTCAGCTGT	TCCAACGTGT
33151	TTACCTGAGG	TACCAGGAAT	GGTGACCTCT	CTGGTTGCTA	GTTCTAGGGC
33201	AGTAACCAGT	ACAACTCTTC	CAACTCTGAC	TCTTTCTCCT	GGTGAACCAG
33251	AGACCACACC	TTCAATGGCC	ACCAGTCATG	GGGCAGAAGC	CAGCTCAACT
33301	GTTCCAACCTG	TTTCACCTGA	GGTACCAGGA	GTGGTGACCT	CTCTGGTCAC
33351	TAGTTCTAGT	GGAGTAAACA	GTACAAGTAT	TCCAACCTCTG	ATTCTTTCTC
33401	CTGGTGAACT	AGAAACCACA	CCTTCAATGG	CCACCAGTCA	TGGGGCAGAA
33451	GCCAGCTCAG	CTGTTCCAAC	TCCAACGTGT	TCACCTGGGG	TATCAGGAGT
33501	GGTGACCCCT	CTGGTCACTA	GTTCCAGGGC	AGTGACCAGT	ACAACTATTTC
33551	CAATTCTAAC	TCTTTCTTCT	AGTGAGCCAG	AGACCACACC	TTCAATGGCC
33601	ACCAGTCATG	GGGTAGAAGC	CAGCTCAGCT	GTTCTAACTG	TTTCACCTGA
33651	GGTACCAGGA	ATGGTGACCT	CTCTGGTCAC	TAGTTCTAGA	GCAGTAACCA
33701	GTACAACTAT	TCCAACCTCTG	ACTATTTCTT	CTGATGAACC	AGAGACCACA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

33751	ACTTCATTGG	TCACCCATTC	TGAGGCAAAG	ATGATTTCAG	CCATTCCAAC
33801	TTTAGCTGTC	TCCCCTACTG	TACAAGGGCT	GGTGACTTCA	CTGGTCACTA
33851	GTTCTGGGTC	AGAGACCAAGT	GCGTTTTTCAA	ATCTAACTGT	TGCCTCAAGT
33901	CAACCAGAGA	CCATAGACTC	ATGGGTCGCT	CATCCTGGGA	CAGAAGCAAG
33951	TTCTGTTGTT	CCAAC TTGA	CTGTCTCCAC	TGGTGAGCCG	TTTACAAATA
34001	TCTCATTGGT	CACCCATCCT	GCAGAGAGTA	GCTCAACTCT	TCCCAGGACA
34051	ACCTCAAGGT	TTTCCCACAG	TGAATTAGAC	ACTATGCCTT	CTACAGTCAC
34101	CAGTCCTGAG	GCAGAATCCA	GCTCAGCCAT	TTCAACTACT	ATTTACCTG
34151	GTATACCAGG	TGTGCTGACA	TCACTGGTCA	CTAGCTCTGG	GAGAGACATC
34201	AGTGCAACTT	TTCCAACAGT	GCCTGAGTCC	CCACATGAAT	CAGAGGCAAC
34251	AGCCTCATGG	GTTACTCATC	CTGCAGTCAC	CAGCACAACA	GTTCCCAGGA
34301	CAACCCCTAA	TTATTCTCAT	AGTGAACCAG	ACACCACACC	ATCAATAGCC
34351	ACCAGTCCTG	GGGCAGAAGC	CACTTCAGAT	TTTCCAACAA	TAACTGTCTC
34401	ACCTGATGTA	CCAGATATGG	TAACCTCACA	GGTCACTAGT	TCTGGGACAG
34451	ACACCAGTAT	AACTATTCCA	ACTCTGACTC	TTTCTTCTGG	TGAGCCAGAG
34501	ACCACAACCT	CATTTATCAC	CTATTCTGAG	ACACACACAA	GTTCAGCCAT
34551	TCCAAC TCTC	CCTGTCTCCC	CTGGTGCATC	AAAGATGCTG	ACCTCACTGG
34601	TCATCAGTTC	TGGGACAGAC	AGCACTACAA	CTTTCCCAAC	ACTGACGGAG
34651	ACCCCATATG	AACCAGAGAC	AACAGCCATA	CAGCTCATTC	ATCCTGCAGA
34701	GACCAACACA	ATGGTTCCCA	AGACAACTCC	CAAGTTTTTCC	CATAGTAAGT
34751	CAGACACCAC	ACTCCCAGTA	GCCATCACCA	GTCCTGGGCC	AGAAGCCAGT
34801	TCAGCTGTTT	CAACGACAAC	TATCTCACCT	GATATGTCAG	ATCTGGTGAC
34851	CTCACTGGTC	CCTAGTTCTG	GGACAGACAC	CAGTACAACC	TTCCCAACAT
34901	TGAGTGAGAC	CCCATATGAA	CCAGAGACTA	CAGTCACGTG	GCTCACTCAT
34951	CCTGCAGAAA	CCAGCACAAC	GGTTTCTGGG	ACAATTCCCA	ACTTTTCCCA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

35001 TAGGGGATCA GACACTGCAC CCTCAATGGT CACCAGTCCT GGAGTAGACA
35051 CGAGGTCAGG TGTTCCTCACT ACAACCATCC CACCCAGTAT ACCAGGGGTA
35101 GTGACCTCAC AGGTCCTAG TTCTGCAACA GACACTAGTA CAGCTATTCC
35151 AACTTTGACT CCTTCTCCTG GTGAACCAGA GACCACAGCC TCATCAGCTA
35201 CCCATCCTGG GACACAGACT GGCTTCACTG TTCCAATTCG GACTGTTCCC
35251 TCTAGTGAGC CAGATACAAT GGCTTCCTGG GTCACATC CTCCACAGAC
35301 CAGCACACCT GTTTCAGAA CAACCTCCAG TTTTCCCAT AGTAGTCCAG
35351 ATGCCACACC TGTAATGGCC ACCAGTCCTA GGACAGAAGC CAGTTCAGCT
35401 GTACTGACAA CAATCTCACC TGGTGCACCA GAGATGGTGA CTTCACAGAT
35451 CACTAGTTCT GGGGAGCAA CCAGTACAAC TGTTCCTCACT TTGACTCATT
35501 CTCCTGGTAT GCCAGAGACC ACAGCCTTAT TGAGCACCCA TCCCAGAACAA
35551 GGGACAAGTA AAACATTTCC TGCTTCACT GTGTTTCCTC AAGTATCAGA
35601 GACCACAGCC TCACTACCA TTAGACCTGG TGCAGAGACT AGCACAGCTC
35651 TCCCAACTCA GACAACATCC TCTCTCTTCA CCCTACTTGT AACTGGAACC
35701 AGCAGAGTTG ATCTAAGTCC AACTGCTTCA CCTGGTGTTT CTGCAAAAAC
35751 AGCCCCACTT TCCACCCATC CAGGGACAGA GACCAGCACA ATGATTCCAA
35801 CTTCAACTCT TTCCCTTGGT TTAGTAGAGA CTACAGGCTT ACTGGCCACC
35851 AGCTCTTCAG CAGAGACCAG CACGAGTACT CTAACCTCTGA CTGTTTCCCC
35901 TGCTGTCTCT GGGCTTTCCA GTGCCTCTAT AACAACTGAT AAGCCCCAAA
35951 CTGTGACCTC CTGGAACACA GAAACCTCAC CATCTGTAAC TTCAGTTGGA
36001 CCCCCAGAAT TTTCCAGGAC TGTCACAGGC ACCACTATGA CCTTGATACC
36051 ATCAGAGATG CCAACACCAC CTAAAACCAG TCATGGAGAA GGAGTGAGTC
36101 CAACCACTAT CTTGAGAACT ACAATGGTTG AAGCCACTAA TTAGCTACC
36151 ACAGGTCCA GTCCCACTGT GGCCAAGACA ACAACCACCT TCAATACACT
36201 GGCTGGAAGC CTCTTTACTC CTCTGACCAC ACCTGGGATG TCCACCTTGG

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

36251	CCTCTGAGAG	TGTGACCTCA	AGAACAAGTT	ATAACCATCG	GTCTTGATC
36301	TCCACCACCA	GCAGTTATAA	CCGTCGGTAC	TGGACCCCTG	CCACCAGCAC
36351	TCCAGTGACT	TCTACATTCT	CCCCAGGGAT	TTCCACATCC	TCCATCCCCA
36401	GCTCCACAGC	AGCCACAGTC	CCATTCATGG	TGCCATTAC	CCTCAACTTC
36451	ACCATCACCA	ACCTGCAGTA	CGAGGAGGAC	ATGCGGCACC	CTGGTTCCAG
36501	GAAGTTCAAC	GCCACAGAGA	GAGAACTGCA	GGGTCTGCTC	AAACCCTTGT
36551	TCAGGAATAG	CAGTCTGGAA	TACCTCTATT	CAGGCTGCAG	ACTAGCCTCA
36601	CTCAGGCCAG	AGAAGGATAG	CTCAGCCATG	GCAGTGGATG	CCATCTGCAC
36651	ACATCGCCCT	GACCCTGAAG	ACCTCGGACT	GGACAGAGAG	CGACTGTACT
36701	GGGAGCTGAG	CAATCTGACA	AATGGCATCC	AGGAGCTGGG	CCCCTACACC
36751	CTGGACCGGA	ACAGTCTCTA	TGTCAATGGT	TTCACCCATC	GAAGCTCTAT
36801	GCCCACCACC	AGCACTCCTG	GGACCTCCAC	AGTGGATGTG	GGAACCTCAG
36851	GGACTCCATC	CTCCAGCCCC	AGCCCCACGG	CTGCTGGCCC	TCTCCTGATG
36901	CCGTTACCCC	TCAACTTCAC	CATCACCAAC	CTGCAGTACG	AGGAGGACAT
36951	GCGTCGCACT	GGCTCCAGGA	AGTTCAACAC	CATGGAGAGT	GTCTGTCAGG
37001	GTCTGCTCAA	GCCCTTGTTT	AAGAACACCA	GTGTTGGCCC	TCTGTACTCT
37051	GGCTGCAGAT	TGACCTTGCT	CAGGCCCGAG	AAAGATGGGG	CAGCCACTGG
37101	AGTGGATGCC	ATCTGCACCC	ACCGCCTTGA	CCCCAAAAGC	CCTGGACTCA
37151	ACAGGGAGCA	GCTGTACTGG	GAGCTAAGCA	AACTGACCAA	TGACATTGAA
37201	GAGCTGGGCC	CCTACACCCT	GGACAGGAAC	AGTCTCTATG	TCAATGGTTT
37251	CACCCATCAG	AGCTCTGTGT	CCACCACCAG	CACTCCTGGG	ACCTCCACAG
37301	TGGATCTCAG	AACCTCAGGG	ACTCCATCCT	CCCTCTCCAG	CCCCACAATT
37351	ATGGCTGCTG	GCCCTCTCCT	GGTACCATTC	ACCCTCAACT	TCACCATCAC
37401	CAACCTGCAG	TATGGGGAGG	ACATGGGTCA	CCCTGGCTCC	AGGAAGTTCA
37451	ACACCACAGA	GAGGGTCCTG	CAGGGTCTGC	TTGGTCCCAT	ATTCAAGAAC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

37501	ACCAGTGTG	GCCCTCTGTA	CTCTGGCTGC	AGACTGACCT	CTCTCAGGTC
37551	TGAGAAGGAT	GGAGCAGCCA	CTGGAGTGGA	TGCCATCTGC	ATCCATCATC
37601	TTGACCCCAA	AAGCCCTGGA	CTCAACAGAG	AGCGGCTGTA	CTGGGAGCTG
37651	AGCCAACTGA	CCAATGGCAT	CAAAGAGCTG	GGCCCCTACA	CCCTGGACAG
37701	GAACAGTCTC	TATGTCAATG	GTTTCACCCA	TCGGACCTCT	GTGCCCACCA
37751	CCAGCACTCC	TGGGACCTCC	ACAGTGGACC	TTGGAACCTC	AGGGACTCCA
37801	TTCTCCCTCC	CAAGCCCCGC	AACTGCTGGC	CCTCTCCTGG	TGCTGTTTAC
37851	CCTCAACTTC	ACCATCACCA	ACCTGAAGTA	TGAGGAGGAC	ATGCATCGCC
37901	CTGGCTCCAG	GAAGTTCAAC	ACCACTGAGA	GGGTCCTGCA	GACTCTGCTT
37951	GGTCCTATGT	TCAAGAACAC	CAGTGTGGC	CTTCTGTACT	CTGGCTGCAG
38001	ACTGACCTTG	CTCAGGTCCG	AGAAGGATGG	AGCAGCCACT	GGAGTGGATG
38051	CCATCTGCAC	CCACCGTCTT	GACCCCAAAA	GCCCTGGACT	GGACAGAGAG
38101	CAGCTATACT	GGGAGCTGAG	CCAGCTGACC	AATGGCATCA	AAGAGCTGGG
38151	CCCCTACACC	CTGGACAGGA	ACAGTCTCTA	TGTCAATGGT	TTCACCCATT
38201	GGATCCCTGT	GCCCACCAGC	AGCACTCCTG	GGACCTCCAC	AGTGGACCTT
38251	GGGTCAGGGA	CTCCATCCTC	CCTCCCCAGC	CCCACAGCTG	CTGGCCCTCT
38301	CCTGGTGCCA	TTCACCCTCA	ACTTCACCAT	CACCAACCTG	CAGTACGAGG
38351	AGGACATGCA	TCACCCAGGC	TCCAGGAAGT	TCAACACCAC	GGAGCGGGTC
38401	CTGCAGGGTC	TGCTTGGTCC	CATGTTCAAG	AACACCAGTG	TCGGCCTTCT
38451	GTA CTCTGGC	TGCAGACTGA	CCTTGCTCAG	GTCCGAGAAG	GATGGAGCAG
38501	CCACTGGAGT	GGATGCCATC	TGCACCCACC	GTCTTGACCC	CAAAAGCCCT
38551	GGAGTGGACA	GGGAGCAGCT	ATACTGGGAG	CTGAGCCAGC	TGACCAATGG
38601	CATCAAAGAG	CTGGGTCCCT	ACACCCTGGA	CAGAAACAGT	CTCTATGTCA
38651	ATGGTTTCAC	CCATCAGACC	TCTGCGCCCA	ACACCAGCAC	TCCTGGGACC
38701	TCCACAGTGG	ACCTGGGGAC	CTCAGGGACT	CCATCCTCCC	TCCCCAGCCC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

38751	TACATCNGCT	GGCCCTCTCC	TGGTNCCNTT	CACCCTCAAC	TTCACCATCA
38801	CCAACCTGCA	GTACGAGGAG	GACATGCGGC	ACCCNGGNTC	CAGGAAGTTC
38851	AACACCACNG	AGAGGGTNCT	GCAGGGTCTG	CTNAAGCCCC	TNTTCAAGAG
38901	CACCAGTGTT	GGCCCTCTGT	ACTCTGGCTG	CAGACTGACC	TTGCTCAGGT
38951	CCGAGAAGGA	TGGAGCAGCC	ACTGGAGTGG	ATGCCATCTG	CACCCACCGT
39001	CTTGACCCCA	AAAGCCCTGG	AGTGGACAGG	GAGCAGCTAT	ACTGGGAGCT
39051	GAGCCAGCTG	ACCAATGGCA	TCAAAGAGCT	GGGTCCCTAC	ACCCTGGACA
39101	GAAACAGTCT	CTATGTCAAT	GGTTTCACCC	ATCAGACCTC	TGCGCCCAAC
39151	ACCAGCACTC	CTGGGACCTC	CACAGTGGAC	CTTGGGACCT	CAGGGACTCC
39201	ATCCTCCCTC	CCCAGCCCTA	CATCTGCTGG	CCCTCTCCTG	GTGCCATTCA
39251	CCCTCAACTT	CACCATCACC	AACCTGCAGT	ACGAGGAGGA	CATGCATCAC
39301	CCAGGCTCCA	GGAAGTTCAA	CACCACGGAG	CGGGTCCTGC	AGGGTCTGCT
39351	TGGTCCCATG	TTCAAGAACA	CCAGTGTCCG	CCTTCTGTAC	TCTGGCTGCA
39401	GA CTGACCTT	GCTCAGGCCT	GAGAAGAATG	GGGCAGCCAC	TGGAATGGAT
39451	GCCATCTGCA	GCCACCGTCT	TGACCCCAA	AGCCCTGGAC	TCAACAGAGA
39501	GCAGCTGTAC	TGGGAGCTGA	GCCAGCTGAC	CCATGGCATC	AAAGAGCTGG
39551	GCCCCTACAC	CCTGGACAGG	AACAGTCTCT	ATGTCAATGG	TTTCACCCAT
39601	CGGAGCTCTG	TGGCCCCCAC	CAGCACTCCT	GGGACCTCCA	CAGTGGACCT
39651	TGGGACCTCA	GGGACTCCAT	CCTCCCTCCC	CAGCCCCACA	ACAGCTGTTC
39701	CTCTCCTGGT	GCCGTTACAC	CTCAACTTTA	CCATCACCAA	TCTGCAGTAT
39751	GGGGAGGACA	TGCGTCACCC	TGGCTCCAGG	AAGTTCAACA	CCACAGAGAG
39801	GGTCCTGCAG	GGTCTGCTTG	GTCCCTTGTT	CAAGAACTCC	AGTGTCGGCC
39851	CTCTGTACTC	TGGCTGCAGA	CTGATCTCTC	TCAGGTCTGA	GAAGGATGGG
39901	GCAGCCACTG	GAGTGGATGC	CATCTGCACC	CACCACCTTA	ACCCTCAAAG
39951	CCCTGGACTG	GACAGGGAGC	AGCTGTACTG	GCAGCTGAGC	CAGATGACCA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

40001	ATGGCATCAA	AGAGCTGGGC	CCCTACACCC	TGGACCGGAA	CAGTCTCTAC
40051	GTCAATGGTT	TCACCCATCG	GAGCTCTGGG	CTCACCACCA	GCACTCCTTG
40101	GACTTCCACA	GTTGACCTTG	GAACCTCAGG	GACTCCATCC	CCCGTCCCCA
40151	GCCCCACAAC	TGCTGGCCCT	CTCCTGGTGC	CATTCACCCT	CAACTTCACC
40201	ATCACCAACC	TGCAGTATGA	GGAGGACATG	CATCGCCCTG	GATCTAGGAA
40251	GTTCAACACC	ACAGAGAGGG	TCCTGCAGGG	TCTGCTTAGT	CCCATTTTCA
40301	AGAACTCCAG	TGTTGGCCCT	CTGTACTCTG	GCTGCAGACT	GACCTCTCTC
40351	AGGCCCGAGA	AGGATGGGGC	AGCAACTGGA	ATGGATGCTG	TCTGCCTCTA
40401	CCACCCTAAT	CCCAAAAGAC	CTGGACTGGA	CAGAGAGCAG	CTGTACTGGG
40451	AGCTAAGCCA	GCTGACCCAC	AACATCACTG	AGCTGGGCCC	CTACAGCCTG
40501	GACAGGGACA	GTCTCTATGT	CAATGGTTTC	ACCCATCAGA	ACTCTGTGCC
40551	CACCACCAGT	ACTCCTGGGA	CCTCCACAGT	GTACTGGGCA	ACCACTGGGA
40601	CTCCATCCTC	CTTCCCCGGC	CACACAGAGC	CTGGCCCTCT	CCTGATACCA
40651	TTCACTTTCA	ACTTTACCAT	CACCAACCTG	ATTATGAGG	AAAACATGCA
40701	ACACCCTGGT	TCCAGGAAGT	TCAACACCAC	GGAGAGGGTT	CTGCAGGGTC
40751	TGCTCAAGCC	CTTGTTCAAG	AACACCAGTG	TTGGCCCTCT	GTACTCTGGC
40801	TGCAGACTGA	CCTCTCTCAG	GCCCGAGAAG	GATGGGGCAG	CAACTGGAAT
40851	GGATGCTGTC	TGCCTCTACC	ACCCTAATCC	CAAAAGACCT	GGGCTGGACA
40901	GAGAGCAGCT	GTACTGGGAG	CTAAGCCAGC	TGACCCACAA	CATCACTGAG
40951	CTGGGCCCCCT	ACAGCCTGGA	CAGGGACAGT	CTCTATGTCA	ATGGTTTCAC
41001	CCATCAGAAC	TCTGTGCCCA	CCACCAGTAC	TCCTGGGACC	TCCACAGTGT
41051	ACTGGGCAAC	CACTGGGACT	CCATCCTCCT	TCCCCGGCCA	CACAGAGCCT
41101	GGCCCTCTCC	TGATACCAT	CACTTTCAAC	TTTACCATCA	CCAACCTGCA
41151	TTATGAGGAA	AACATGCAAC	ACCCTGGTTC	CAGGAAGTTC	AACACCACGG
41201	AGAGGGTTCT	GCAGGGTCTG	CTCAAGCCCT	TGTTCAAGAA	CACCAGTGTT

Table 4 (continued)

Human cDNA of CA125

(SEQ ID NO: 4)

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41251  GGCCCTCTGT ACTCTGGCTG CAGACTGACC TTGCTCAGAC CTGAGAAGCA
41301  TGAGGCAGCC ACTGGAGTGG ACACCATCTG TACCCACCGC GTTGATCCCA
41351  TCGGACCTGG ACTGGACAGG GAGCGGCTAT ACTGGGAGCT GAGCCAGCTG
41401  ACCAACAGCA TTACCGAACT GGGACCCTAC ACCCTGGACA GGGACAGTCT
41451  CTATGTCAAT GGCTTCAACC CTCGGAGCTC TGTGCCAACC ACCAGCACTC
41501  CTGGGACCTC CACAGTGCAC CTGGCAACCT CTGGGACTCC ATCCTCCCTG
41551  CCTGGCCACA CAGCCCCCTGT CCCTCTCTTG ATACCATTCA CCCTCAACTT
41601  TACCATCACC AACCTGCATT ATGAGGAAAA CATGCAACAC CCTGGTTCCA
41651  GGAAGTTCAA CACCACGGAG AGGGTTCTGC AGGGTCTGCT CAAGCCCTTG
41701  TTCAAGAACA CCAGTGTGG CCCTCTGTAC TCTGGCTGCA GACTGACCTT
41751  GCTCAGACCT GAGAAGCATG AGGCAGCCAC TGGAGTGGAC ACCATCTGTA
41801  CCCACCGCGT TGATCCCATC GGACCTGGAC TGNACAGNGA GCNGCTNTAC
41851  TGGGAGCTNA GCCANCTGAC CAANNNCATC NNGAGCTGG GNCCCTACAC
41901  CCTGGACAGG NACAGTCTCT ATGTCAATGG TTTCACCCAT CNGANCTCTG
41951  NGCCCACCAC CAGCACTCCT GGGACCTCCA CAGTGNACNT NGGNACCTCN
42001  GGGACTCCAT CCTCCNTCCC CNGCCNCACA TCTGCTGGCC CTCTCCTGGT
42051  GCCATTCACC CTCAACTTCA CCATCACCAA CCTGCAGTAC GAGGAGGACA
42101  TGCATCACCC AGGCTCCAGG AAGTTCAACA CCACGGAGCG GGTCTGTCAG
42151  GGTCTGCTTG GTCCCATGTT CAAGAACACC AGTGTGCGCC TTCTGTACTC
42201  TGGCTGCAGA CTGACCTTGC TCAGGCCTGA GAAGAATGGG GCAGCCACTG
42251  GAATGGATGC CATCTGCAGC CACCGTCTTG ACCCCAAAAG CCCTGGACTC
42301  GACAGAGAGC AGCTGTACTG GGAGCTGAGC CAGCTGACCC ATGGCATCAA
42351  AGAGCTGGGC CCCTACACCC TGGACAGGAA CAGTCTCTAT GTCAATGGTT
42401  TCACCCATCG GAGCTCTGTG GCCCCACCA GCACTCCTGG GACCTCCACA
42451  GTGGACCTTG GGACCTCAGG GACTCCATCC TCCCTCCCCA GCCCCACAAC

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Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

42501	AGCTGTTCCCT	CTCCTGGTGC	CGTTCACCCT	CAACTTTACC	ATCACCAATC
42551	TGCAGTATGG	GGAGGACATG	CGTCACCCTG	GCTCCAGGAA	GTTCAACACC
42601	ACAGAGAGGG	TCCTGCAGGG	TCTGCTTGGT	CCCTTGTTCA	AGAACTCCAG
42651	TGTCGGCCCT	CTGTACTCTG	GCTGCAGACT	GATCTCTCTC	AGGTCTGAGA
42701	AGGATGGGGC	AGCCACTGGA	GTGGATGCCA	TCTGCACCCA	CCACCTTAAC
42751	CCTCAAAGCC	CTGGACTGGA	CAGGGAGCAG	CTGTACTGGC	AGCTGAGCCA
42801	GATGACCAAT	GGCATCAAAG	AGCTGGGCCC	CTACACCCTG	GACCGGAACA
42851	GTCTCTACGT	CAATGGTTTC	ACCCATCGGA	GCTCTGGGCT	CACCACCAGC
42901	ACTCCTTGGA	CTTCCACAGT	TGACCTTGGA	ACCTCAGGGA	CTCCATCCCC
42951	CGTCCCCAGC	CCCACAACCTG	CTGGCCCTCT	CCTGGTGCCA	TTCACCCTAA
43001	ACTTCACCAT	CACCAACCTG	CAGTATGAGG	AGGACATGCA	TCGCCCTGGA
43051	TCTAGGAAGT	TCAACGCCAC	AGAGAGGGTC	CTGCAGGGTC	TGCTTAGTCC
43101	CATATTCAAG	AACTCCAGTG	TTGGCCCTCT	GTACTCTGGC	TGCAGACTGA
43151	CCTCTCTCAG	GCCCGAGAAG	GATGGGGCAG	CAACTGGAAT	GGATGCTGTC
43201	TGCCTCTACC	ACCCTAATCC	CAAAAGACCT	GGACTGGACA	GAGAGCAGCT
43251	GTA CTGGGAG	CTAAGCCAGC	TGACCCACAA	CATCACTGAG	CTGGGCCCCT
43301	ACAGCCTGGA	CAGGGACAGT	CTCTATGTCA	ATGGTTTCAC	CCATCAGAGC
43351	TCTATGACGA	CCACCAGAAC	TCCTGATACC	TCCACAATGC	ACCTGGCAAC
43401	CTCGAGAACT	CCAGCCTCCC	TGTCTGGACC	TACGACCGCC	AGCCCTCTCC
43451	TGGTGCTATT	CACAATCAAC	TGCACCATCA	CCAACCTGCA	GTACGAGGAG
43501	GACATGCGTC	GCACTGGCTC	CAGGAAGTTC	AACACCATGG	AGAGTGTCTT
43551	GCAGGGTCTG	CTCAAGCCCT	TGTTCAAGAA	CACCAGTGTT	GGCCCTCTGT
43601	ACTCTGGCTG	CAGATTGACC	TTGCTCAGGC	CCAAGAAAGA	TGGGGCAGCC
43651	ACTGGAGTGG	ATGCCATCTG	CACCCACCGC	CTTGACCCCA	AAAGCCCTGG
43701	ACTCAACAGG	GAGCAGCTGT	ACTGGGAGCT	AAGCAAACCTG	ACCAATGACA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

43751	TTGAAGAGCT	GGGCCCCTAC	ACCCTGGACA	GGAACAGTCT	CTATGTCAAT
43801	GGTTTCACCC	ATCAGAGCTC	TGTGTCCACC	ACCAGCACTC	CTGGGACCTC
43851	CACAGTGGAT	CTCAGAACCT	CAGGGACTCC	ATCCTCCCTC	TCCAGCCCCA
43901	CAATTATGNC	NNCTGNCCCT	CTCCTGNTNC	CNTTCACCNT	CAACTTNACC
43951	ATCACCAACC	TGCANTANGN	GGANNACATG	CNNCNCNCNG	GNTCCAGGAA
44001	GTTCAACACC	ACNGAGAGGG	TCCTACAGGG	TCTGCTCAGG	CCCTTGTTCA
44051	AGAACACCAG	TGTCAGCTCT	CTGTACTCTG	GTTGCAGACT	GACCTTGCTC
44101	AGGCCTGAGA	AGGATGGGGC	AGCCACCAGA	GTGGATGCTG	CCTGCACCTA
44151	CCGCCCTGAT	CCCAAAAGCC	CTGGACTGGA	CAGAGAGCAA	CTATACTGGG
44201	AGCTGAGCCA	GCTAACCAC	AGCATCACTG	AGCTGGGACC	CTACACCCTG
44251	GACAGGGTCA	GTCTCTATGT	CAATGGCTTC	AACCCTCGGA	GCTCTGTGCC
44301	AACCACCAGC	ACTCCTGGGA	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA
44351	CTCCATCCTC	CCTGCCTGGC	CACACANCNN	CTGNCCCTCT	CCTGNTNCCN
44401	TTCACCNTCA	ACTTNACCAT	CACCAACCTG	CANTANGNGG	ANNACATGCN
44451	NCNCCCNGGN	TCCAGGAAGT	TCAACACCAC	NGAGAGGGTT	CTGCAGGGTC
44501	TGCTCAAACC	CTTGTTTCAGG	AATAGCAGTC	TGGAATACCT	CTATTCAGGC
44551	TGCAGACTAG	CCTCACTCAG	GCCAGAGAAG	GATAGCTCAG	CCATGGCAGT
44601	GGATGCCATC	TGCACACATC	GCCCTGACCC	TGAAGACCTC	GGACTGGACA
44651	GAGAGCGACT	GTACTGGGAG	CTGAGCAATC	TGACAAATGG	CATCCAGGAG
44701	CTGGGCCCCCT	ACACCCTGGA	CCGGAACAGT	CTCTACGTCA	ATGGTTTCAC
44751	CCATCGGAGC	TCTGGGCTCA	CCACCAGCAC	TCCTTGGACT	TCCACAGTTG
44801	ACCTTGGAAC	CTCAGGGACT	CCATCCCCCG	TCCCCAGCCC	CACAACTGCT
44851	GGCCCTCTCC	TGGTGCCATT	CACCCTCAAC	TTCACCATCA	CCAACCTGCA
44901	GTATGAGGAG	GACATGCATC	GCCCTGGTTC	CAGGAGGTTC	AACACCACGG
44951	AGAGGGTTCT	GCAGGGTCTG	CTCACGCCCT	TGTTCAAGAA	CACCAGTGTT

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

45001	GGCCCTCTGT	ACTCTGGCTG	CAGACTGACC	TTGCTCAGAC	CTGAGAAGCA
45051	AGAGGCAGCC	ACTGGAGTGG	ACACCATCTG	TACCCACCGC	GTTGATCCCA
45101	TCGGACCTGG	ACTGGACAGA	GAGCGGCTAT	ACTGGGAGCT	GAGCCAGCTG
45151	ACCAACAGCA	TCACAGAGCT	GGGACCCTAC	ACCCTGGATA	GGGACAGTCT
45201	CTATGTCAAT	GGCTTCAACC	CTTGGAGCTC	TGTGCCAACC	ACCAGCACTC
45251	CTGGGACCTC	CACAGTGCAC	CTGGCAACCT	CTGGGACTCC	ATCCTCCCTG
45301	CCTGGCCACA	CAGCCCCTGT	CCCTCTCTTG	ATACCATTCA	CCCTCAACTT
45351	TACCATCACC	GACCTGCATT	ATGAAGAAAA	CATGCAACAC	CCTGGTTCCA
45401	GGAAGTTCAA	CACCACGGAG	AGGGTTCTGC	AGGGTCTGCT	CAAGCCCTTG
45451	TTCAAGAGCA	CCAGCGTTGG	CCCTCTGTAC	TCTGGCTGCA	GACTGACCTT
45501	GCTCAGACCT	GAGAAACATG	GGGCAGCCAC	TGGAGTGGAC	GCCATCTGCA
45551	CCCTCCGCCT	TGATCCCACT	GGTCCTGGAC	TGGACAGAGA	GCGGCTATAC
45601	TGGGAGCTGA	GCCAGCTGAC	CAACAGCGTT	ACAGAGCTGG	GCCCCTACAC
45651	CCTGGACAGG	GACAGTCTCT	ATGTCAATGG	CTTCACCCAT	CGGAGCTCTG
45701	TGCCAACCAC	CAGTATTCTT	GGGACCTCTG	CAGTGCACCT	GGAAACCTCT
45751	GGGACTCCAG	CCTCCCTCCC	TGGCCACACA	GCCCCTGGCC	CTCTCCTGGT
45801	GCCATTCAAC	CTCAACTTCA	CTATCACCAA	CCTGCAGTAT	GAGGAGGACA
45851	TGCGTCACCC	TGGTTCCAGG	AAGTTCAGCA	CCACGGAGAG	AGTCCTGCAG
45901	GGTCTGCTCA	AGCCCTTGTT	CAAGAACACC	AGTGTGAGCT	CTCTGTACTC
45951	TGGTTGCAGA	CTGACCTTGC	TCAGGCCTGA	GAAGGATGGG	GCAGCCACCA
46001	GAGTGGATGC	TGTCTGCACC	CATCGTCCTG	ACCCCAAAAG	CCCTGGACTG
46051	GACAGAGAGC	GGCTGTACTG	GAAGCTGAGC	CAGCTGACCC	ACGGCATCAC
46101	TGAGCTGGGC	CCCTACACCC	TGGACAGGCA	CAGTCTCTAT	GTCAATGGTT
46151	TCACCCATCA	GAGCTCTATG	ACGACCACCA	GAACCTCCTGA	TACCTCCACA
46201	ATGCACCTGG	CAACCTCGAG	AACTCCAGCC	TCCCTGTCTG	GACCTACGAC

Table 4 (continued)

 Human cDNA of CA125
 (SEQ ID NO: 4)

46251	CGCCAGCCCT	CTCCTGGTGC	TATTCACAAT	TAAC TTCACC	ATCACTAACC
46301	TGCGGTATGA	GGAGAACATG	CATCACCCCTG	GCTCTAGAAA	GTTTAACACC
46351	ACGGAGAGAG	TCCTTCAGGG	TCTGCTCAGG	CCTGTGTTCA	AGAACACCAG
46401	TGTTGGCCCT	CTGTACTCTG	GCTGCAGACT	GACCACGCTC	AGGCCCAAGA
46451	AGGATGGGGC	AGCCACCAAA	GTGGATGCCA	TCTGCACCTA	CCGCCCTGAT
46501	CCCAAAGCC	CTGGACTGGA	CAGAGAGCAG	CTATACTGGG	AGCTGAGCCA
46551	GCTAACCAC	AGCATCACTG	AGCTGGGCCC	CTACACCCAG	GACAGGGACA
46601	GTCTCTATGT	CAATGGCTTC	ACCCATCGGA	GCTCTGTGCC	AACCACCAGT
46651	ATTCCTGGGA	CCTCTGCAGT	GCACCTGGAA	ACCTCTGGGA	CTCCAGCCTC
46701	CCTCCCTGGC	CACACAGCCC	CTGGCCCTCT	CCTGGTGCCA	TTCACCCTCA
46751	ACTTCACTAT	CACCAACCTG	CAGTATGAGG	AGGACATGCG	TCACCCTGGT
46801	TCCAGGAAGT	TCAACACCAC	GGAGAGAGTC	CTGCAGGGTC	TGCTCAAGCC
46851	CTTGTTCAAG	AGCACCAGTG	TTGGCCCTCT	GTA CTCTGGC	TGCAGACTGA
46901	CCTTGCTCAG	GCCTGAAAAA	CGTGGGGCAG	CCACCGGCGT	GGACACCATC
46951	TGCACTCACC	GCCTTGACCC	TCTAAACCCA	GGACTGGACA	GAGAGCAGCT
47001	ATACTGGGAG	CTGAGCAAAC	TGACCCGTGG	CATCATCGAG	CTGGGCCCCCT
47051	ACCTCCTGGA	CAGAGGCAGT	CTCTATGTCA	ATGGTTTCAC	CCATCGGACC
47101	TCTGTGCCCA	CCACCAGCAC	TCCTGGGACC	TCCACAGTGG	ACCTTGGAAC
47151	CTCAGGGACT	CCATTCTCCC	TCCAAGCCC	CGCANCNNCT	GNCCCTCTCC
47201	TGNTNCCNTT	CACNTCAAC	TTNACCATCA	CCAACCTGCA	NTANGNGGAN
47251	NACATGCNNC	NCCNNGGNTC	CAGGAAGTTC	AACACCACNG	AGAGGGTCCT
47301	GCAGACTCTG	CTTGGTCCTA	TGTTCAAGAA	CACCAGTGTT	GGCCTTCTGT
47351	ACTCTGGCTG	CAGACTGACC	TTGCTCAGGT	CCGAGAAGGA	TGGAGCAGCC
47401	ACTGGAGTGG	ATGCCATCTG	CACCCACCGT	CTTGACCCCA	AAAGCCCTGG
47451	AGTGGACAGG	GAGCAACTAT	ACTGGGAGCT	GAGCCAGCTG	ACCAATGGCA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

47501	TTAAAGAACT	GGGCCCCTAC	ACCCTGGACA	GGAACAGTCT	CTATGTCAAT
47551	GGGTTCACCC	ATTGGATCCC	TGTGCCCACC	AGCAGCACTC	CTGGGACCTC
47601	CACAGTGGAC	CTTGGGTCAG	GGACTCCATC	CTCCCTCCCC	AGCCCCACAA
47651	CTGCTGGCCC	TCTCCTGGTG	CCGTTACCCC	TCAACTTCAC	CATCACCAAC
47701	CTGAAGTACG	AGGAGGACAT	GCATTGCCCT	GGCTCCAGGA	AGTTCAACAC
47751	CACAGAGAGA	GTCCTGCAGA	GTCTGCTTGG	TCCCATGTTC	AAGAACACCA
47801	GTGTTGGCCC	TCTGTACTCT	GGCTGCAGAC	TGACCTTGCT	CAGGTCCGAG
47851	AAGGATGGAG	CAGCCACTGG	AGTGGATGCC	ATCTGCACCC	ACCGTCTTGA
47901	CCCCAAAAGC	CCTGGAGTGG	ACAGGGAGCA	GCTATACTGG	GAGCTGAGCC
47951	AGCTGACCAA	TGGCATCAAA	GAGCTGGGTC	CCTACACCCT	GGACAGAAAC
48001	AGTCTCTATG	TCAATGGTTT	CACCCATCAG	ACCTCTGCGC	CCAACACCAG
48051	CACTCCTGGG	ACCTCCACAG	TGGACCTTGG	GACCTCAGGG	ACTCCATCCT
48101	CCCTCCCCAG	CCCTACANCN	NCTGNCCCTC	TCCTGNTNCC	NTTCACCNTC
48151	AACTTNACCA	TCACCAACCT	GCANTANGNG	GANNACATGC	NNCNCCCNGG
48201	NTCCAGGAAG	TTCAACACCA	CNGAGNGNGT	NCTGCAGGGT	CTGCTNNNNC
48251	CCNTNTTCAA	GAACNCCAGT	GTNGGCCNTC	TGTA CTCTGG	CTGCAGACTG
48301	ACCTNNCTCA	GGNCNGAGAA	GNATGGNGCA	GCCACTGGAN	TGGATGCCAT
48351	CTGCANCEAG	CNNCNTNANC	CCAAAAGNCC	TGGACTGNAC	AGNGAGCNGC
48401	TN TACTGGGA	GCTNAGCCAN	CTGACCAANN	NCATCNNNGA	GCTGGGNCCC
48451	TACACCCTGG	ACAGGNACAG	TCTCTATGTC	AATGGTTTCA	CCCATTGGAT
48501	CCCTGTGCCC	ACCAGCAGCA	CTCCTGGGAC	CTCCACAGTG	GACCTTGGGT
48551	CAGGGACTCC	ATCCTCCCTC	CCCAGCCCCA	CAACTGCTGG	CCCTCTCCTG
48601	GTGCCGTTCA	CCCTCAACTT	CACCATCACC	AACCTGAAGT	ACGAGGAGGA
48651	CATGCATTGC	CCTGGCTCCA	GGAAGTTCAA	CACCACAGAG	AGAGTCCTGC
48701	AGAGTCTGCT	TGGTCCCATG	TTCAAGAACA	CCAGTGTGG	CCCTCTGTAC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

48751	TCTGGCTGCA	GACTGACCTC	GCTCAGGTCC	GAGAAGGATG	GAGCAGCCAC
48801	TGGAGTGGAT	GCCATCTGCA	CCCACCGTGT	TGACCCCAAA	AGCCCTGGAG
48851	TGGACAGGGA	GCAGCTATAC	TGGGAGCTGA	GCCAGCTGAC	CAATGGCATC
48901	AAAGAGCTGG	GTCCCTACAC	CCTGGACAGA	AACAGTCTCT	ATGTCAATGG
48951	TTTCACCCAT	CAGACCTCTG	CGCCCAACAC	CAGCACTCCT	GGGACCTCCA
49001	CAGTGNACNT	NGGNACCTCN	GGGACTCCAT	CCTCCNTCCC	CNGCCNCACA
49051	TCTGCTGGCC	CTCTCCTGGT	GCCATTCACC	CTCAACTTCA	CCATCACCAA
49101	CCTGCAGTAC	GAGGAGGACA	TGCATCACCC	AGGCTCCAGG	AAGTTCAACA
49151	CCACGGAGCG	GGTCCTGCAG	GGTCTGCTTG	GTCCCATGTT	CAAGAACACC
49201	AGTGTGGGCC	TTCTGTACTC	TGGCTGCAGA	CTGACCTTGC	TCAGGCCTGA
49251	GAAGAATGGG	GCAACCACTG	GAATGGATGC	CATCTGCACC	CACCGTCTTG
49301	ACCCCAAAAG	CCCTGGACTG	NACAGNGAGC	NGCTNTACTG	GGAGCTNAGC
49351	CANCTGACCA	ANNNCATCNN	NGAGCTGGGN	CCCTACACCC	TGGACAGGNA
49401	CAGTCTCTAT	GTCAATGGTT	TCACCCATCN	GANCTCTGNG	CCCACCACCA
49451	GCACTCCTGG	GACCTCCACA	GTGNACNTNG	GNACCTCNGG	GACTCCATCC
49501	TCCNTCCCCN	GCCNCACANC	NNCTGNCCCT	CTCCTGNTNC	CNTTCACCNT
49551	CAACTTNACC	ATCACCAACC	TGCANTANGN	GGANNACATG	CNNCNCNCNG
49601	GNTCCAGGAA	GTTCAACACC	ACNGAGAGGG	TTCTGCAGGG	TCTGCTCAAA
49651	CCCTTGTTCA	GGAATAGCAG	TCTGGAATAC	CTCTATTGAG	GCTGCAGACT
49701	AGCCTCACTC	AGGCCAGAGA	AGGATAGCTC	AGCCATGGCA	GTGGATGCCA
49751	TCTGCACACA	TCGCCCTGAC	CCTGAAGACC	TCGGACTGGA	CAGAGAGCGA
49801	CTGTACTGGG	AGCTGAGCAA	TCTGACAAAT	GGCATCCAGG	AGCTGGGCCC
49851	CTACACCCTG	GACCGGAACA	GTCTCTATGT	CAATGGTTTC	ACCCATCGAA
49901	GCTCTATGCC	CACCACCAGC	ACTCCTGGGA	CCTCCACAGT	GGATGTGGGA
49951	ACCTCAGGGA	CTCCATCCTC	CAGCCCCAGC	CCCACGACTG	CTGGCCCTCT

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

50001	CCTGATACCA	TTCACCCTCA	ACTTCACCAT	CACCAACCTG	CAGTATGGGG
50051	AGGACATGGG	TCACCCTGGC	TCCAGGAAGT	TCAACACCAC	AGAGAGGGTC
50101	CTGCAGGGTC	TGCTTGGTCC	CATATTCAAG	AACACCAGTG	TTGGCCCTCT
50151	GTACTCTGGC	TGCAGACTGA	CCTCTCTCAG	GTCTGAGAAG	GATGGAGCAG
50201	CCACTGGAGT	GGATGCCATC	TGCATCCATC	ATCTTGACCC	CAAAAGCCCT
50251	GGACTCAACA	GAGAGCGGCT	GTACTGGGAG	CTGAGCCAAC	TGACCAATGG
50301	CATCAAAGAG	CTGGGCCCCCT	ACACCCTGGA	CAGGAACAGT	CTCTATGTCA
50351	ATGGTTTCAC	CCATCGGACC	TCTGTGCCCA	CCACCAGCAC	TCCTGGGACC
50401	TCCACAGTGG	ACCTTGGAAC	CTCAGGGACT	CCATTCTCCC	TCCAAGCCC
50451	CGCAACTGCT	GGCCCTCTCC	TGGTGCTGTT	CACCCTCAAC	TTCACCATCA
50501	CCAACCTGAA	GTATGAGGAG	GACATGCATC	GCCCTGGCTC	CAGGAAGTTC
50551	AACACCACTG	AGAGGGTCCT	GCAGACTCTG	CTTGGTCCTA	TGTTCAAGAA
50601	CACCAGTGTT	GGCCTTCTGT	ACTCTGGCTG	CAGACTGACC	TTGCTCAGGT
50651	CCGAGAAGGA	TGGAGCAGCC	ACTGGAGTGG	ATGCCA TCTG	CACCCACCGT
50701	CTTGACCCCA	AAAGCCCTGG	ACTGNACAGN	GAGCNGCTNT	ACTGGGAGCT
50751	NAGCCANCTG	ACCAANNNCA	TCNNNGAGCT	GGNCCCTAC	ACCCTGGACA
50801	GGNACAGTCT	CTATGTCAAT	GGTTTCACCC	ATCNGANCTC	TGN G C C C A C C
50851	ACCAGCACTC	CTGGGACCTC	CACAGTGNAC	NTNGGNACCT	CN G G G A C T C C
50901	ATCCTCCNTC	CCCN G C C N C A	CAN CN N C T G N	CCCTCTCCTG	NTN C C N T T C A
50951	CCNTCAACTT	NACCATCACC	AACCTGCANT	ANGNGGANNA	CATGCNNCNC
51001	CCNGGNTCCA	GGAAGTTCAA	CACCACNGAG	AGAGTCCTTC	AGGGTCTGCT
51051	CAGGCCTGTG	TTCAAGAACA	CCAGTGTTGG	CCCTCTGTAC	TCTGGCTGCA
51101	GACTGACCTT	GCTCAGGCCC	AAGAAGGATG	GGGCAGCCAC	CAAAGTGGAT
51151	GCCATCTGCA	CCTACCGCCC	TGATCCCAAA	AGCCCTGGAC	TGGACAGAGA
51201	GCAGCTATAC	TGGGAGCTGA	GCCAGCTAAC	CCACAGCATC	ACTGAGCTGG

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

51251	GCCCCTACAC	CCAGGACAGG	GACAGTCTCT	ATGTCAATGG	CTTCACCCAT
51301	CGGAGCTCTG	TGCCAACCAC	CAGTATTCCT	GGGACCTCTG	CAGTGCACCT
51351	GGAAACCACT	GGGACTCCAT	CCTCCTTCCC	CGGCCACACA	GAGCCTGGCC
51401	CTCTCCTGAT	ACCATTCACT	TTCAACTTTA	CCATCACCAA	CCTGCGTTAT
51451	GAGGAAAACA	TGCAACACCC	TGGTTCCAGG	AAGTTCAACA	CCACGGAGAG
51501	GGTTCTGCAG	GGTCTGCTCA	CGCCCTTGTT	CAAGAACACC	AGTGTGGGCC
51551	CTCTGTACTC	TGGCTGCAGA	CTGACCTTGC	TCAGACCTGA	GAAGCAGGAG
51601	GCAGCCACTG	GAGTGGACAC	CATCTGTACC	CACCGCGTTG	ATCCCATCGG
51651	ACCTGGACTG	GACAGAGAGC	GGCTATACTG	GGAGCTGAGC	CAGCTGACCA
51701	ACAGCATCAC	AGAGCTGGGA	CCCTACACCC	TGGATAGGGA	CAGTCTCTAT
51751	GTCGATGGCT	TCAACCCTTG	GAGCTCTGTG	CCAACCACCA	GCACTCCTGG
51801	GACCTCCACA	GTGCACCTGG	CAACCTCTGG	GACTCCATCC	CCCCTGCCTG
51851	GCCACACAGC	CCCTGTCCCT	CTCTTGATAC	CATTCACCCT	CAACTTTACC
51901	ATCACCGACC	TGCATTATGA	AGAAAACATG	CAACACCCTG	GTTCCAGGAA
51951	GTTCAACACC	ACGGAGAGGG	TTCTGCAGGG	TCTGCTCAAG	CCCTTGTTCA
52001	AGAGCACCAG	CGTTGGCCCT	CTGTACTCTG	GCTGCAGACT	GACCTTGCTC
52051	AGACCTGAGA	AACATGGGGC	AGCCACTGGA	GTGGACGCCA	TCTGCACCCT
52101	CCGCCTTGAT	CCCACTGGTC	CTGGACTGGA	CAGAGAGCGG	CTATACTGGG
52151	AGCTGAGCCA	GCTGACCAAC	AGCATCACAG	AGCTGGGACC	CTACACCCTG
52201	GATAGGGACA	GTCTCTATGT	CAATGGCTTC	AACCCTTGGA	GCTCTGTGCC
52251	AACCACCAGC	ACTCCTGGGA	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA
52301	CTCCATCCTC	CCTGCCTGGC	CACACAAC TG	CTGGCCCTCT	CCTGGTGCCG
52351	TTCACCCTCA	ACTTCACCAT	CACCAACCTG	AAGTACGAGG	AGGACATGCA
52401	TTGCCCTGGC	TCCAGGAAGT	TCAACACCAC	AGAGAGAGTC	CTGCAGAGTC
52451	TGCATGGTCC	CATGTTCAAG	AACACCAGTG	TTGGCCCTCT	GTA CTCTGGC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

52501	TGCAGACTGA	CCTTGCTCAG	GTCCGAGAAG	GATGGAGCAG	CCACTGGAGT
52551	GGATGCCATC	TGCACCCACC	GTCTTGACCC	CAAAAGCCCT	GGACTGNACA
52601	GNGAGCNGCT	NTACTGGGAG	CTNAGCCANC	TGACCAANNN	CATCNNNGAG
52651	CTGGGNCCCT	ACACCCTGGA	CAGGNACAGT	CTCTATGTCA	ATGGTTTCAC
52701	CCATCNGANC	TCTGNGCCCA	CCACCAGCAC	TCCTGGGACC	TCCACAGTGN
52751	ACNTNGGNAC	CTCNGGGACT	CCATCCTCCN	TCCCCNGCCN	CACANCNNCT
52801	GNCCCTCTCC	TGNTNCCNTT	CACCNTCAAC	TTNACCATCA	CCAACCTGCA
52851	NTANGNGGAN	NACATGCNNC	NCCCNGGNTC	CAGGAAGTTC	AACACCACNG
52901	AGNGNGTNCT	GCAGGGTCTG	CTNNNNCCCN	TNTTCAAGAA	CNCCAGTGTN
52951	GGCNTCTGT	ACTCTGGCTG	CAGACTGACC	TNNCTCAGGN	CNGAGAAGNA
53001	TGGNGCAGCC	ACTGGANTGG	ATGCCATCTG	CANCCACCNN	CNTNANCCCA
53051	AAAGNCCTGG	ACTGNACAGN	GAGCNGCTNT	ACTGGGAGCT	NAGCCANCTG
53101	ACCAACAGCA	TCACAGAGCT	GGGACCCCTAC	ACCCTGGATA	GGGACAGTCT
53151	CTATGTCAAT	GGTTTCACCC	ATCGAAGCTC	TATGCCCACC	ACCAGTATTC
53201	CTGGGACCTC	TGCAGTGCAC	CTGGAACCT	CTGGGACTCC	AGCCTCCCTC
53251	CCTGGCCACA	CAGCCCCTGG	CCCTCTCCTG	GTGCCATTCA	CCCTCAACTT
53301	CACTATCACC	AACCTGCAGT	ATGAGGAGGA	CATGCGTCAC	CCTGGTTCCA
53351	GGAAGTTCAA	CACCACGGAG	AGAGTCCTGC	AGGGTCTGCT	CAAGCCCTTG
53401	TTCAAGAGCA	CCAGTGTTGG	CCCTCTGTAC	TCTGGCTGCA	GACTGACCTT
53451	GCTCAGGCCT	GAAAAACGTG	GGGCAGCCAC	CGGCGTGGAC	ACCATCTGCA
53501	CTCACCGCCT	TGACCCTCTA	AACCCTGGAC	TGNACAGNGA	GCNGCTNTAC
53551	TGGGAGCTNA	GCCANCTGAC	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC
53601	CCTGGACAGG	NACAGTCTCT	ATGTCAATGG	TTTCACCCAT	CNGANCTCTG
53651	NGCCCACCAC	CAGCACTCCT	GGGACCTCCA	CAGTGNACNT	NGGNACCTCN
53701	GGGACTCCAT	CCTCCNTCCC	CNGCCNCACA	NCNNCTGNCC	CTCTCCTGNT

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

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53751 NCCNTTCACC NTCAACTTNA CCATCACCAA CCTGCANTAN GNGGANNACA
53801 TGCNNCNCNC NGGNTCCAGG AAGTTCAACA CCACNGAGNG NGTNCTGCAG
53851 GGTCTGCTNN NNCCNTNTT CAAGAACNCC AGTGTNGGCC NTCTGTACTC
53901 TGGCTGCAGA CTGACCTNNC TCAGGNCNGA GAAGNATGGN GCAGCCACTG
53951 GANTGGATGC CATCTGCANC CACCNNCNTN ANCCCAAAG NCCTGGACTG
54001 NACAGNGAGC NGCTNTACTG GGAGCTNAGC CANCTGACCA ANNNCATCNN
54051 NGAGCTGGGN CCCTACACCC TGGACAGGNA CAGTCTCTAT GTCAATGGTT
54101 TTCACCTCG GAGCTCTGTG CCAACCACCA GCACTCCTGG GACCTCCACA
54151 GTGCACCTGG CAACCTCTGG GACTCCATCC TCCCTGCCTG GCCACACAGC
54201 CCCTGTCCCT CTCTTGATAC CATTACCCCT CAACTTTACC ATCACCAACC
54251 TGCATTATGA AGAAAACATG CAACACCCTG GTTCCAGGAA GTTCAACACC
54301 ACGGAGCGGG TCCTGCAGGG TCTGCTTGGT CCCATGTTCA AGAACACAAG
54351 TGTGGGCTT CTGTACTCTG GCTGCAGACT GACCTTGCTC AGGCCTGAGA
54401 AGAATGGGGC AGCCACTGGA ATGGATGCCA TCTGCAGCCA CCGTCTTGAC
54451 CCCAAAAGCC CTGGACTGNA CAGNGAGCNG CTNTACTGGG AGCTNAGCCA
54501 NCTGACCAAN NNCATCMNNG AGCTGGGNCC CTACACCCTG GACAGGNACA
54551 GTCTCTATGT CAATGGTTTC ACCCATCNGA NCTCTGNGCC CACCACCAGC
54601 ACTCCTGGGA CCTCCACAGT GNACNTNGGN ACCTCNGGGA CTCCATCCTC
54651 CNTCCCCNGC CNCACANCNN CTGNCCCTCT CCTGNTNCCN TTCACNTCA
54701 ACTTNACCAT CACCAACCTG CANTANGNGG ANNACATGCN NCNCCNNGN
54751 TCCAGGAAGT TCAACACCAC NGAGNGNGTN CTGCAGGGTC TGCTNNNNCC
54801 CNTNTTCAAG AACNCCAGTG TNGGCCNTCT GTACTCTGGC TGCAGACTGA
54851 CCTNNCTCAG GNCNGAGAAG NATGGNGCAG CCACTGGANT GGATGCCATC
54901 TGCANCCACC NNCNTNANCC CAAAAGNCCT GGACTGNACA GNGAGCNGCT
54951 NTA CTGGGAG CTNAGCCANC TGACCAANNN CATCNNNGAG CTGGGNCCCT

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Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

55001	ACACCCTGGA	CAGGNACAGT	CTCTATGTCA	ATGGTTTCAC	CCATCAGAAC
55051	TCTGTGCCCA	CCACCAGTAC	TCCTGGGACC	TCCACAGTGT	ACTGGGCAAC
55101	CACTGGGACT	CCATCCTCCT	TCCCCGGCCA	CACAGAGCCT	GGCCCTCTCC
55151	TGATACCATT	CACTTTCAAC	TTTACCATCA	CCAACCTGCA	TTATGAGGAA
55201	AACATGCAAC	ACCCTGGTTC	CAGGAAGTTC	AACACCACGG	AGAGGGTTCT
55251	GCAGGGTCTG	CTCACGCCCT	TGTTCAAGAA	CACCAGTGTT	GGCCCTCTGT
55301	ACTCTGGCTG	CAGACTGACC	TTGCTCAGAC	CTGAGAAGCA	GGAGGCAGCC
55351	ACTGGAGTGG	ACACCATCTG	TACCCACCGC	GTTGATCCCA	TCGGACCTGG
55401	ACTGNACAGN	GAGCNGCTNT	ACTGGGAGCT	NAGCCANCTG	ACCAANNNCA
55451	TCNNNGAGCT	GGNCCCCTAC	ACCCTGGACA	GGNACAGTCT	CTATGTCAAT
55501	GGTTTCACCC	ATCNGANCTC	TGNGCCCACC	ACCAGCACTC	CTGGGACCTC
55551	CACAGTGNAC	NTNGGNACCT	CNGGGACTCC	ATCCTCCNTC	CCCNGCCNCA
55601	CANCNNCTGN	CCCTCTCCTG	NTNCCNTTCA	CCNTCAACTT	NACCATCACC
55651	AACCTGCANT	ANGNGGANNA	CATGCNNCNC	CCNGGNTCCA	GGAAGTTCAA
55701	CACCACNGAG	NGNGTNCTGC	AGGGTCTGCT	NNNNCCCNTN	TTCAAGAACN
55751	CCAGTGTTGG	CCNTCTGTAC	TCTGGCTGCA	GACTGACCTN	NCTCAGGNCN
55801	GAGAAGNATG	GNGCAGCCAC	TGGANTGGAT	GCCATCTGCA	NCCACCNNCN
55851	TNANCCCAAA	AGNCCTGGAC	TGNACAGNGA	GCNGCTNTAC	TGGGAGCTNA
55901	GCCANCTGAC	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC	CCTGGACAGG
55951	NACAGTCTCT	ATGTCAATGG	TTTCACCCAT	CGGAGCTCTG	TGCCAACCAC
56001	CAGCAGTCCT	GGGACCTCCA	CAGTGCACCT	GGCAACCTCT	GGGACTCCAT
56051	CCTCCCTGCC	TGGCCACACA	GCCCCTGTCC	CTCTCTTGAT	ACCATTCACC
56101	CTCAACTTTA	CCATCACCAA	CCTGCATTAT	GAAGAAAACA	TGCAACACCC
56151	TGGTTCAGG	AAGTTCAACA	CCACGGAGAG	GGTTCTGCAG	GGTCTGCTCA
56201	AGCCCTTGTT	CAAGAGCACC	AGTGTGGGCC	CTCTGTACTC	TGGCTGCAGA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

56251	CTGACCTTGC	TCAGACCTGA	GAAACATGGG	GCAGCCACTG	GAGTGGACGC
56301	CATCTGCACC	CTCCGCCTTG	ATCCCACTGG	TCCTGGACTG	NACAGNGAGC
56351	NGCTNTACTG	GGAGCTNAGC	CANCTGACCA	ANNNCATCNN	NGAGCTGGGN
56401	CCCTACACCC	TGGACAGGNA	CAGTCTCTAT	GTCAATGGTT	TCACCCATCN
56451	GANCTCTGNG	CCCACCACCA	GCACTCCTGG	GACCTCCACA	GTGNACNTNG
56501	GNACCTCNGG	GACTCCATCC	TCCNTCCCN	GCCNCACANC	NNCTGNCCCT
56551	CTCCTGNTNC	CNTTCACCNT	CAACTTNACC	ATCACCAACC	TGCANTANGN
56601	GGANNACATG	CNNCNCNCNG	GNTCCAGGAA	GTTCAACACC	ACNGAGNGNG
56651	TNCTGCAGGG	TCTGCTNNNN	CCCNTNTTCA	AGAACNCCAG	TGTNGGCCNT
56701	CTGTACTCTG	GCTGCAGACT	GACCTNNCTC	AGGNCNGAGA	AGNATGGNGC
56751	AGCCACTGGA	NTGGATGCCA	TCTGCANCCA	CCNNCNTNAN	CCCAAAGNC
56801	CTGGACTGNA	CAGNGAGCNG	CTNTACTGGG	AGCTNAGCCA	NCTGACCAAN
56851	NNCATCNNNG	AGCTGGGNCC	CTACACCCTG	GACAGGNACA	GTCTCTATGT
56901	CAATGGTTTC	ACCCATCGGA	CCTCTGTGCC	CACCACCAGC	ACTCCTGGGA
56951	CCTCCACAGT	GCACCTGGCA	ACCTCTGGGA	CTCCATCCTC	CCTGCCTGGC
57001	CACACAGCCC	CTGTCCCTCT	CTTGATACCA	TTCACCCTCA	ACTTTACCAT
57051	CACCAACCTG	CAGTATGAGG	AGGACATGCA	TCGCCCTGGA	TCTAGGAAGT
57101	TCAACACCAC	AGAGAGGGTC	CTGCAGGGTC	TGCTTAGTCC	CATTTTCAAG
57151	AACTCCAGTG	TTGGCCCTCT	GTACTCTGGC	TGCAGACTGA	CCTCTCTCAG
57201	GCCCGAGAAG	GATGGGGCAG	CAACTGGAAT	GGATGCTGTC	TGCCTCTACC
57251	ACCCTAATCC	CAAAAGACCT	GGGCTGGACA	GAGAGCAGCT	GTA CTGCGAG
57301	CTAAGCCAGC	TGACCCACAA	CATCACTGAG	CTGGGCCCCT	ACAGCCTGGA
57351	CAGGGACAGT	CTCTATGTCA	ATGGTTTCAC	CCATCAGAAC	TCTGTGCCCCA
57401	CCACCAGTAC	TCCTGGGACC	TCCACAGTGT	ACTGGGCAAC	CACTGGGACT
57451	CCATCCTCCT	TCCCCGGCCA	CACANCNNCT	GNCCCTCTCC	TGNTNCCNTT

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

57501	CACCNTCAAC	TTNACCATCA	CCAACCTGCA	NTANGNGGAN	NACATGCNNC
57551	NCCCNGGNTC	CAGGAAGTTC	AACACCACNG	AGNGNGTNCT	GCAGGGTCTG
57601	CTNNNNCCCN	TNTTCAAGAA	CNCCAGTGTN	GGCCNTCTGT	ACTCTGGCTG
57651	CAGACTGACC	TNNCTCAGGN	CNGAGAAGNA	TGGNGCAGCC	ACTGGANTGG
57701	ATGCCATCTG	CANCCACCNN	CNTNANCCCA	AAAGNCCTGG	ACTGNACAGN
57751	GAGCNGCTNT	ACTGGGAGCT	NAGCCANCTG	ACCAANNNCA	TCNNNGAGCT
57801	GGGNCCCTAC	ACCCTGGACA	GGNACAGTCT	CTATGTCAAT	GGTTTCACCC
57851	ATTGGAGCTC	TGGGCTCACC	ACCAGCACTC	CTTGGACTTC	CACAGTTGAC
57901	CTTGGAACCT	CAGGGACTCC	ATCCCCCGTC	CCCAGCCCCA	CAACTGCTGG
57951	CCCTCTCCTG	GTGCCATTCA	CCCTAAACTT	CACCATCACC	AACCTGCAGT
58001	ATGAGGAGGA	CATGCATCGC	CCTGGATCTA	GGAAGTTCAA	CGCCACAGAG
58051	AGGGTCCTGC	AGGGTCTGCT	TAGTCCCATA	TTCAAGAACA	CCAGTGTTGG
58101	CCCTCTGTAC	TCTGGCTGCA	GA CTGACCTT	GCTCAGACCT	GAGAAGCAGG
58151	AGGCAGCCAC	TGGAGTGGAC	ACCATCTGTA	CCCACCGCGT	TGATCCCATC
58201	GGACCTGGAC	TGNACAGNGA	GCNGCTNTAC	TGGGAGCTNA	GCCANCTGAC
58251	CAANNNCATC	NNNGAGCTGG	GNCCCTACAC	CCTGGACAGG	NACAGTCTCT
58301	ATGTCAATGG	TTTCACCCAT	CNGANCTCTG	NGCCCACCAC	CAGCACTCCT
58351	GGGACCTCCA	CAGTGNACNT	NGGNACCTCN	GGGACTCCAT	CCTCCNTCCC
58401	CNGCCNCACA	NCNNCTGNCC	CTCTCCTGNT	NCCNTTCACC	NTCAACTTNA
58451	CCATCACCAA	CCTGCANTAN	GNGGANNACA	TGCNNCNCCC	NGGNTCCAGG
58501	AAGTTCAACA	CCACNGAGNG	NGTNCTGCAG	GGTCTGCTNN	NNCCCNTNTT
58551	CAAGAACNCC	AGTGTNGGCC	NTCTGTACTC	TGGCTGCAGA	CTGACCTNNC
58601	TCAGGNCNGA	GAAGNATGGN	GCAGCCACTG	GANTGGATGC	CATCTGCANC
58651	CACCNNCNTN	ANCCCAAAAG	NCCTGGACTG	NACAGNGAGC	NGCTNTACTG
58701	GGAGCTNAGC	CANCTGACCA	ANNNCATCNN	NGAGCTGGGN	CCCTACACCC

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

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58751  TGGACAGGNA CAGTCTCTAT GTCAATGGTT TCACCCATCG GAGCTTTGGG
58801  CTCACCACCA GCACTCCTTG GACTTCCACA GTTGACCTTG GAACCTCAGG
58851  GACTCCATCC CCCGTCCCCA GCCCCACAAC TGCTGGCCCT CTCCTGGTGC
58901  CATTCACCCT AAAC TTCACC ATCACCAACC TGCAGTATGA GGAGGACATG
58951  CATCGCCCTG GCTCCAGGAA GTTCAACACC ACGGAGAGGG TCCTTCAGGG
59001  TCTGCTTACG CCCTTGTTCA GGAACACCAG TGTGAGCTCT CTGTACTCTG
59051  GTTGCAGACT GACCTTGCTC AGGCCTGAGA AGGATGGGGC AGCCACCAGA
59101  GTGGATGCTG TCTGCACCCA TCGTCCTGAC CCCAAAAGCC CTGGACTGNA
59151  CAGNGAGCNG CTN TACTGGG AGCTNAGCCA NCTGACCAAN NNCATC N NNG
59201  AGCTGGGNCC CTACACCCTG GACAGGNACA GTCTCTATGT CAATGGTTTC
59251  ACCCATCNGA NCTCTGNGCC CACCACCAGC ACTCCTGGGA CCTCCACAGT
59301  GNACNTNGGN ACCTCNGGGA CTCCATCCTC CNTCCCCNGC CNCACANCNN
59351  CTGNCCCTCT CCTGNTNCCN TTCACCNTCA ACTTNACCAT CACCAACCTG
59401  CANTANGNGG ANNACATGCN NCNCCCNGGN TCCAGGAAGT TCAACACCAC
59451  NGAGNGNGTN CTGCAGGGTC TGCTNNNNCC CNTNTTCAAG AACNCCAGTG
59501  TNGGCCNTCT GTACTCTGGC TGCAGACTGA CCTNNCTCAG GNCNGAGAAG
59551  NATGGNGCAG CCACTGGANT GGATGCCATC TGCANCCACC NNCNTNANCC
59601  CAAAAGNCCT GGA CTGNACA GNGAGCNGCT NTACTGGGAG CTNAGCCANC
59651  TGACCAANNN CATCNNGAG CTGGGNCCCT ACACCCTGGA CAGGNACAGT
59701  CTCTATGTCA ATGGTTTCAC CCATTGGATC CCTGTGCCA CCAGCAGCAC
59751  TCCTGGGACC TCCACAGTGG ACCTTGGGTC AGGGACTCCA TCCTCCCTCC
59801  CCAGCCCCAC AACTGCTGGC CCTCTCCTGG TACCATTAC CCTCAACTTC
59851  ACCATCACCA ACCTGCAGTA TGGGGAGGAC ATGGGTCACC CTGGCTCCAG
59901  GAAGTTCAAC ACCACAGAGA GGGTCCTGCA GGGTCTGCTT GGTCCCATAT
59951  TCAAGAACAC CAGTGTTGGC CCTCTGTACT CTGGCTGCAG ACTGACCTCT

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Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

60001	CTCAGGTCCG	AGAAGGATGG	AGCAGCCACT	GGAGTGGATG	CCATCTGCAT
60051	CCATCATCTT	GACCCCAAAA	GCCCTGGACT	GNACAGNGAG	CNGCTNTACT
60101	GGGAGCTNAG	CCANCTGACC	AANNNCATCN	NNGAGCTGGG	NCCCTACACC
60151	CTGGACAGGN	ACAGTCTCTA	TGTCAATGGT	TTCACCCATC	NGANCTCTGN
60201	GCCCACCACC	AGCACTCCTG	GGACCTCCAC	AGTGNACNTN	GGNACCTCNG
60251	GGACTCCATC	CTCCNTCCCC	NGCCNCACAN	CNNCTGNCCC	TCTCCTGNTN
60301	CCNTTCACCN	TCAACTTNAC	CATCACCAAC	CTGCANTANG	NGGANNACAT
60351	GCNNCNCCCN	GGNTCCAGGA	AGTTCAACAC	CACNGAGNGN	GTNCTGCAGG
60401	GTCTGCTNNN	NCCCNTNTTC	AAGAACNCCA	GTGTNGGCCN	TCTGTACTCT
60451	GGCTGCAGAC	TGACCTNNCT	CAGGNCNGAG	AAGNATGGNG	CAGCCACTGG
60501	ANTGGATGCC	ATCTGCANCC	ACCNNCNTNA	NCCCAAAAGN	CCTGGACTGN
60551	ACAGNGAGCN	GCTNTACTGG	GAGCTNAGCC	ANCTGACCAA	NNNCATCNNN
60601	GAGCTGGGNC	CCTACACCCT	GGACAGGNAC	AGTCTCTATG	TCAATGGTTT
60651	CACCCATCAG	ACCTTTGCGC	CCAACACCAG	CACTCCTGGG	ACCTCCACAG
60701	TGGACCTTGG	GACCTCAGGG	ACTCCATCCT	CCCTCCCCAG	CCCTACATCT
60751	GCTGGCCCTC	TCCTGGTGCC	ATTCACCCTC	AACTTCACCA	TCACCAACCT
60801	GCAGTACGAG	GAGGACATGC	ATCACCAGG	CTCCAGGAAG	TTCAACACCA
60851	CGGAGCGGGT	CCTGCAGGGT	CTGCTTGGTC	CCATGTTCAA	GAACACCAGT
60901	GTCGGCCTTC	TGTACTCTGG	CTGCAGACTG	ACCTTGCTCA	GGCCTGAGAA
60951	GAATGGGGCA	GCCACCAGAG	TGGATGCTGT	CTGCACCCAT	CGTCCTGACC
61001	CCAAAAGCCC	TGGACTGNAC	AGNGAGCNGC	TNTACTGGGA	GCTNAGCCAN
61051	CTGACCAANN	NCATCNNNGA	GCTGGGNCCC	TACACCCTGG	ACAGGNACAG
61101	TCTCTATGTC	AATGGTTTCA	CCCATCNGAN	CTCTGNGCCC	ACCACCAGCA
61151	CTCCTGGGAC	CTCCACAGTG	NACNTNGGNA	CCTCNGGGAC	TCCATCCTCC
61201	NTCCCCNGCC	NCACAGCCCC	TGTCCCTCTC	TTGATACCAT	TCAECCTCAA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

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61251 CTTTACCATC ACCAACCTGC ATTATGAAGA AAACATGCAA CACCCTGGTT
61301 CCAGGAAGTT CAACACCACG GAGAGGGTTC TGCAGGGTCT GCTCAAGCCC
61351 TTGTTCAAGA GCACCAGCGT TGGCCCTCTG TACTCTGGCT GCAGACTGAC
61401 CTTGCTCAGA CCTGAGAAAC ATGGGGCAGC CACTGGAGTG GACGCCATCT
61451 GCACCCTCCG CCTTGATCCC ACTGGTCCTG GACTGGACAG AGAGCGGCTA
61501 TACTGGGAGC TGAGCCAGCT GACCAACAGC GTTACAGAGC TGGGCCCCTA
61551 CACCCTGGAC AGGGACAGTC TCTATGTCAA TGGCTTCACC CAGCGGAGCT
61601 CTGTGCCAAC CACCAGTATT CCTGGGACCT CTGCAGTGCA CCTGGAAACC
61651 TCTGGGACTC CAGCCTCCCT CCCTGGCCAC ACAGCCCCTG GCCCTCTCCT
61701 GGTGCCATT CACCTCAACT TCACTATCAC CAACCTGCAG TATGAGGTGG
61751 ACATGCGTCA CCCTGGTTCC AGGAAGTTCA ACACCACGGA GAGAGTCCTG
61801 CAGGGTCTGC TCAAGCCCTT GTTCAAGAGC ACCAGTGTG GCCCTCTGTA
61851 CTCTGGCTGC AGACTGACCT TGCTCAGGCC TGAAAAACGT GGGGCAGCCA
61901 CCGGCGTGGA CACCATCTGC ACTCACC GCC TTAGACCCTCT AAACCCTGGA
61951 CTGGACAGAG AGCAGCTATA CTGGGAGCTG AGCAAACCTGA CCCGTGGCAT
62001 CATCGAGCTG GGCCCTACC TCCTGGACAG AGGCAGTCTC TATGTCAATG
62051 GTTTCACCCA TCGGAACCTT GTGCCCATCA CCAGCACTCC TGGGACCTCC
62101 ACAGTACACC TAGGAACCTC TGAAACTCCA TCCTCCCTAC CTAGACCCAT
62151 AGTGCCTGGC CCTCTCCTGG TGCCATTAC CCTCAACTTC ACCATCACCA
62201 ACTTGCACTA TGAGGAGGCC ATGCGACACC CTGGCTCCAG GAAGTTCAAT
62251 ACCACGGAGA GGGTCCTACA GGGTCTGCTC AGGCCCTTGT TCAAGAATAC
62301 CAGTATCGGC CCTCTGTACT CCAGCTGCAG ACTGACCTTG CTCAGGCCAG
62351 AGAAGGACAA GGCAGCCACC AGAGTGGATG CCATCTGTAC CCACCACCCT
62401 GACCCTCAAA GCCCTGGACT GAACAGAGAG CAGCTGTACT GGGAGCTGAG
62451 CCAGCTGACC CACGGCATCA CTGAGCTGGG CCCCTACACC CTGGACAGGG

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Table 4 (continued)

 Human cDNA of CA125
 (SEQ ID NO: 4)

62501	ACAGTCTCTA	TGTCGATGGT	TTCACCTCATT	GGAGCCCCAT	ACCGACCACC
62551	AGCACTCCTG	GGACCTCCAT	AGTGAACCTG	GGAACCTCTG	GGATCCCACC
62601	TTCCCTCCCT	GAAACTACAN	CNNCTGNCCC	TCTCCTGNTN	CCNTTCACCN
62651	TCAACTTNAC	CATCACCAAC	CTGCANTANG	NGGANNACAT	GCNNCNCNCCN
62701	GGNTCCAGGA	AGTTCAACAC	CACNGAGAGG	GTTCTGCAGG	GTCTGCTCAA
62751	GCCCTTGTTT	AAGAGCACCA	GTGTTGGCCC	TCTGTATTCT	GGCTGCAGAC
62801	TGACCTTGCT	CAGGCCTGAG	AAGGACGGAG	TAGCCACCAG	AGTGGACGCC
62851	ATCTGCACCC	ACCGCCCTGA	CCCCAAAATC	CCTGGGCTAG	ACAGACAGCA
62901	GCTATACTGG	GAGCTGAGCC	AGCTGACCCA	CAGCATCACT	GAGCTGGGAC
62951	CCTACACCCCT	GGATAGGGAC	AGTCTCTATG	TCAATGGTTT	CACCCAGCGG
63001	AGCTCTGTGC	CCACCACCAG	CACTCCTGGG	ACTTTCACAG	TACAGCCGGA
63051	AACCTCTGAG	ACTCCATCAT	CCCTCCCTGG	CCCCACAGCC	ACTGGCCCTG
63101	TCCTGCTGCC	ATTCACCCTC	AATTTTACCA	TCACTAACCT	GCAGTATGAG
63151	GAGGACATGC	ATCGCCCTGG	CTCCAGGAAG	TTCAACACCA	CGGAGAGGGT
63201	CCTTCAGGGT	CTGCTTATGC	CCTTGTTCAA	GAACACCAGT	GTCAGCTCTC
63251	TGTA CTCTGG	TTGCAGACTG	ACCTTGCTCA	GGCCTGAGAA	GGATGGGGCA
63301	GCCACCAGAG	TGGATGCTGT	CTGCACCCAT	CGTCCTGACC	CCAAAAGCCC
63351	TGGACTGGAC	AGAGAGCGGC	TGTA CTGGAA	GCTGAGCCAG	CTGACCCACG
63401	GCATCACTGA	GCTGGGCCCC	TACACCCTGG	ACAGGCACAG	TCTCTATGTC
63451	AATGGTTTCA	CCCATCAGAG	CTCTATGACG	ACCACCAGAA	CTCCTGATAC
63501	CTCCACAATG	CACCTGGCAA	CCTCGAGAAC	TCCAGCCTCC	CTGTCTGGAC
63551	CTACGACCGC	CAGCCCTCTC	CTGGTGCTAT	TCACAATTAA	CTTCACCATC
63601	ACTAACCTGC	GGTATGAGGA	GAACATGCAT	CACCCTGGCT	CTAGAAAGTT
63651	TAACACCACG	GAGAGAGTCC	TTCAGGGTCT	GCTCAGGCCT	GTGTTCAAGA
63701	ACACCAGTGT	TGGCCCTCTG	TACTCTGGCT	GCAGACTGAC	CTTGCTCAGG

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

63751	CCCAAGAAGG	ATGGGGCAGC	CACCAAAGTG	GATGCCATCT	GCACCTACCG
63801	CCCTGATCCC	AAAAGCCCTG	GACTGGACAG	AGAGCAGCTA	TACTGGGAGC
63851	TGAGCCAGCT	AACCCACAGC	ATCACTGAGC	TGGGCCCCTA	CACCCTGGAC
63901	AGGGACAGTC	TCTATGTCAA	TGGTTTCACA	CAGCGGAGCT	CTGTGCCCAC
63951	CACTAGCATT	CCTGGGACCC	CCACAGTGGG	CCTGGGAACA	TCTGGGACTC
64001	CAGTTTCTAA	ACCTGGTCCC	TCGGCTGCCA	GCCCTCTCCT	GGTGCTATTG
64051	ACTCTCAACT	TCACCATCAC	CAACCTGCGG	TATGAGGAGA	ACATGCAGCA
64101	CCCTGGCTCC	AGGAAGTTCA	ACACCACGGA	GAGGGTCCTT	CAGGGCCTGC
64151	TCAGGTCCCT	GTTCAAGAGC	ACCACTGTTG	GCCCTCTGTA	CTCTGGCTGC
64201	AGACTGACTT	TGCTCAGGCC	TGAAAAGGAT	GGGACAGCCA	CTGGAGTGGG
64251	TGCCATCTGC	ACCCACCACC	CTGACCCCAA	AAGCCCTAGG	CTGGACAGAG
64301	AGCAGCTGTA	TTGGGAGCTG	AGCCAGCTGA	CCCACAATAT	CACTGAGCTG
64351	GGCCACTATG	CCCTGGACAA	CGACAGCCTC	TTTGTCAATG	GTTTCACTCA
64401	TCGGAGCTCT	GTGTCCACCA	CCAGCACTCC	TGGGACCCCC	ACAGTGTATC
64451	TGGGAGCATC	TAAGACTCCA	GCCTCGATAT	TTGGCCCTTC	AGCTGCCAGC
64501	CATCTCCTGA	TACTATTAC	CCTCAACTTC	ACCATCACTA	ACCTGCGGTA
64551	TGAGGAGAAC	ATGTGGCCTG	GCTCCAGGAA	GTTCAACACT	ACAGAGAGGG
64601	TCCTTCAGGG	CCTGCTAAGG	CCCTTGTTCA	AGAACACCAG	TGTTGGCCCT
64651	CTGTACTCTG	GCTCCAGGCT	GACCTTGCTC	AGGCCAGAGA	AAGATGGGGA
64701	AGCCACCGGA	GTGGATGCCA	TCTGCACCCA	CCGCCCTGAC	CCCACAGGCC
64751	CTGGGCTGGA	CAGAGAGCAG	CTGTATTTGG	AGCTGAGCCA	GCTGACCCAC
64801	AGCATCACTG	AGCTGGGCCC	CTACACACTG	GACAGGGACA	GTCTCTATGT
64851	CAATGGTTTC	ACCCATCGGA	GCTCTGTACC	CACCACCAGC	ACCGGGGTGG
64901	TCAGCGAGGA	GCCATTACAA	CTGAACTTCA	CCATCAACAA	CCTGCGCTAC
64951	ATGGCGGACA	TGGGCCAACC	CGGCTCCCTC	AAGTTCAACA	TCACAGACAA

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

65001	CGTCATGAAG	CACCTGCTCA	GTCCTTTGTT	CCAGAGGAGC	AGCCTGGGTG
65051	CACGGTACAC	AGGCTGCAGG	GTCATCGCAC	TAAGGTCTGT	GAAGAACGGT
65101	GCTGAGACAC	GGGTGGACCT	CCTCTGCACC	TACCTGCAGC	CCCTCAGCGG
65151	CCCAGGTCTG	CCTATCAAGC	AGGTGTTCCA	TGAGCTGAGC	CAGCAGACCC
65201	ATGGCATCAC	CCGGCTGGGC	CCCTACTCTC	TGGACAAAGA	CAGCCTCTAC
65251	CTTAACGGTT	ACAATGAACC	TGGTCTAGAT	GAGCCTCCTA	CAACTCCCAA
65301	GCCAGCCACC	ACATTCCTGC	CTCCTCTGTC	AGAAGCCACA	ACAGCCATGG
65351	GGTACCACCT	GAAGACCCTC	AACTCAACT	TCACCATCTC	CAATCTCCAG
65401	TATTCACCAG	ATATGGGCAA	GGGCTCAGCT	ACATTCAACT	CCACCGAGGG
65451	GGTCCTTCAG	CACCTGCTCA	GACCCTTGTT	CCAGAAGAGC	AGCATGGGCC
65501	CCTTCTACTT	GGGTTGCCAA	CTGATCTCCC	TCAGGCCTGA	GAAGGATGGG
65551	GCAGCCACTG	GTGTGGACAC	CACCTGCACC	TACCACCCTG	ACCCTGTGGG
65601	CCCCGGGCTG	GACATACAGC	AGCTTTACTG	GGAGCTGAGT	CAGCTGACCC
65651	ATGGTGTCAC	CCAAGTGGGC	TTCTATGTCC	TGGACAGGGA	TAGCCTCTTC
65701	ATCAATGGCT	ATGCACCCCA	GAATTTATCA	ATCCGGGGCG	AGTACCAGAT
65751	AAATTTCCAC	ATTGTCAACT	GGAACCTCAG	TAATCCAGAC	CCCACATCCT
65801	CAGAGTACAT	CACCCTGCTG	AGGGACATCC	AGGACAAGGT	CACCACACTC
65851	TACAAAGGCA	GTCAACTACA	TGACACATTC	CGTTTCTGCC	TGGTCACCAA
65901	CTTGACGATG	GACTCCGTGT	TGGTCACTGT	CAAGGCATTG	TTCTCCTCCA
65951	ATTTGGACCC	CAGCCTGGTG	GAGCAAGTCT	TTCTAGATAA	GACCCTGAAT
66001	GCCTCATTC	ATTGGCTGGG	CTCCACCTAC	CAGTTGGTGG	ACATCCATGT
66051	GACAGAAATG	GAGTCATCAG	TTTATCAACC	AACAAGCAGC	TCCAGCACCC
66101	AGCACTTCTA	CCTGAATTTT	ACCATCACCA	ACCTACCATA	TTCCAGGAC
66151	AAAGCCCAGC	CAGGCACCAC	CAATTACCAG	AGGAACAAAA	GGAATATTGA
66201	GGATGCGCTC	AACCAACTCT	TCCGAAACAG	CAGCATCAAG	AGTTATTTTT

Table 4 (continued)

Human cDNA of CA125
(SEQ ID NO: 4)

66251	CTGACTGTCA	AGTTTCAACA	TTCAGGTCTG	TCCCCAACAG	GCACCACACC
66301	GGGGTGGACT	CCCTGTGTAA	CTTCTCGCCA	CTGGCTCGGA	GAGTAGACAG
66351	AGTTGCCATC	TATGAGGAAT	TTCTGCGGAT	GACCCGGAAT	GGTACCCAGC
66401	TGCAGAACTT	CACCCTGGAC	AGGAGCAGTG	TCCTTGTGGA	TGGGTATTCT
66451	CCCAACAGAA	ATGAGCCCTT	AACTGGGAAT	TCTGACCTTC	CCTTCTGGGC
66501	TGTCATCCTC	ATCGGCTTGG	CAGGACTCCT	GGGACTCATC	ACATGCCTGA
66551	TCTGCGGTGT	CCTGGTGACC	ACCCGCCGGC	GGAAGAAGGA	AGGAGAATAC
66601	AACGTCCAGC	AACAGTGCCC	AGGCTACTAC	CAGTCACACC	TAGACCTGGA
66651	GGATCTGCAA	TGACTGGAAC	TTGCCGGTGC	CTGGGGTGCC	TTTCCCCCAG
66701	CCAGGGTCCA	AAGAAGCTTG	GCTGGGGCAG	AAATAAACCA	TATTGGTCGG
66751	AAAAAAAAAA	AAAAA			

Table 5

Human Protein of CA125 Molecule
(SEQ ID NO: 5)

1	MLKPSGLPGS	SSPTRSLMTG	SRSTKATPEM	DSGLTGATLS	PKTSTGAIVV
51	TEHTLPFTSP	DKTLASPTSS	VVGRTTQSLG	VMSSALPEST	SRGMTHSEQR
101	TSPSLSPQVN	GTPSRNYPAT	SMVSGLSSPR	TRTSSTEGNF	TKEASTYTLT
151	VETTSGPVTE	KYTVPTETST	TEGDSTETPW	DTRYIPVKIT	SPMKTFADST
201	ASKENAPVSM	TPAETTVTDS	HTPGRTNPSF	GTLYSSFLDL	SPKGTPNRSG
251	ETSLELILST	TGYPFSSPEP	GSAGHSRIST	SAPLSSSASV	LDNKISETSI
301	FSGQSLTSPL	SPGVPEARAS	TMPNSAIPFS	MTLSNAETSA	ERVRSTISSL
351	GTPSISTKQT	AETILTFHAF	AETMDIPSTH	IAKTLASEWL	GSPGTLGGTS
401	TSALTTTSPS	TTLVSEETNT	HHSTSGKETE	GTLNTSMTPL	ETSAPGEESE
451	MTATLVPTLG	FTTLDKIRS	PSQVSSSHPT	RELRTTGSTS	GRQSSSTAAB
501	GSSDILRATT	SSTSKASSWT	SESTAQQFSE	PQHTQWVETS	PSMKTERPPA
551	STSVAAPITT	SVPSVVGFT	TLKTSSTKGI	WLEETSADTL	IGESTAGPTT
601	HQFAVPTGIS	MTGGSSTRGS	QGTTHLLTRA	TASSETSADL	TLATNGVPVS
651	VSPAUSKTAA	GSSPPGGTKP	SYTMVSSVIP	ETSSLQSSAF	REGTSLGLTP
701	LNTRHPFSSP	EPDSAGHTKI	STSIPLLSA	SVLEDKVSAT	STFSHHKATS
751	SITTGTPEIS	TKTKPSSAVL	SSMTLSNAAT	SPERVRNATS	PLTHPSPSGE
801	ETAGSVLTL	TSAETTDSPN	IHPTGTLTSE	SSESPSTLSL	PSVSGVKTF
851	SSSTPSTHLF	TSGEETEETS	NPSVSQPETS	VSRVRTTLAS	TSVPTPVFPT
901	MDTWPTRSAQ	FSSSHLVSEL	RATSSTSVTN	STGSALPKIS	HLTGATMSQ
951	TNRDTFNDSA	APQSTTWPET	SPRFKTGLPS	ATTTVSTSAT	SLSATVMVSK
1001	FTSPATSSME	ATSIREPSTT	ILTTETTNBP	GSMASASTNI	PIGKGYITEG
1051	RLDTSHLPIC	TTASSETSMD	FTMAKESVSM	SVSPSQSMDA	AGSSTPGRTS
1101	QFVDTFSDDV	YHLTSREITI	PRDGTSSALT	PQMTATHPPS	PDPGSARSTW
1151	LGILSSSPSS	PTPKVTMSST	FSTQRVTTSM	IMDTVETSRW	NMPNLPSTTS
1201	LTPSNIPTSG	AIGKSTLVPL	DTPSPATSLE	ASEGGLPTLS	TYPESTNTPS

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
1251	IHLGAHASSE	SPSTINLTMA	SVVKPGSYTP	LTFPSIETHI	HVSTARMAYS
1301	SGSSPEMTAP	GETNTGSTWD	PTYIITTTDP	KDTSSAQVST	PHSVRTLRTT
1351	ENHPKTESAT	PAAYSGSPKI	SSSPNLTSPA	TKAWTITDTT	EHSTQLHYTK
1401	LAEKSSGFET	QSAPGPVSVV	IPTSPTIGSS	TLELTSDVPG	EPLVLAPSEQ
1451	TTITLPMATW	LSTSLTEEMA	STDLDISSPS	SPMSTFAIFP	PMSTPSHEL
1501	KSEADTSAIR	NTDSTTLDQH	LGIRSLGRTG	DLTTVPITPL	TTTWTSVIEH
1551	STQAQDTLSA	TMSPTHVTQS	LKDQTSIPAS	ASPSHLTEVY	PELGTQGRSS
1601	SEATTFWKPS	TDTLREIET	GPTNIQSTPP	MDNTTGGSSS	SGVTLGIAHL
1651	PIGTSSPAET	STNMALERRS	STATVSMAGT	MGLLVTSAPG	RSISQSLGRV
1701	SSVLSESTTE	GVTDSKSGSS	PRLNTQGNTA	LSSSLEPSYA	EGSQMSTSIP
1751	LTSSPTTPDV	EFIGGSTFWT	KEVTTVMTSD	ISKSSARTES	SSATLMSTAL
1801	GSTENTGKEK	LRTASMDLPS	PTPSMEVTPW	ISLTLSNAPN	TTDSLDSLHG
1851	VHTSSAGTLA	TDRSLNTGVT	RASRLENGSD	TSSKSLSMGN	STHTSMTDTE
1901	KSEVSSSIHP	RPETSAPGAE	TTLTSTPGNR	AISLTLPFSS	IPVEEVISTG
1951	ITSGPDINSA	PMTHSPITPP	TIVWTSTGTI	EQSTQPLHAV	SSEKVSQVQTQ
2001	STPYVNSVAV	SASPTHENSV	SSGSSTSSPY	SSASLES LDS	TISRRNAITS
2051	WLWDLTTS LP	TTTWPSTSLS	EALSSGHSGV	SNPSSTTTEF	PLFSAASTSA
2101	AKQRNPETET	HGPQNTAAST	LNTDASSVTG	LSETPVGASI	SSEVPLPMAI
2151	TSRSDVSGLT	SESTANPSLG	TASSAGTKLT	RTISLPTSES	LVSFRMNKDP
2201	WTVSIPLGSH	PTTNTETSIP	VNSAGPPGLS	TVASDVIDTP	SDGAESIPTV
2251	SFSPSPDTEV	TTISHFPEKT	THSFRTISSL	THELTSRVTP	IPGDWMSSAM
2301	STKPTGASPS	ITLGERRTIT	SAAPTTSPIV	LTASF TETST	VSLDNETTVK
2351	TSDILDARKT	NELPSDSSSS	SDLINTSIAS	STMDVTKTAS	ISPTSISGMT
2401	ASSSPSLFSS	DRPQVPTSTT	ETNTATSPSV	SSNTYSLDGG	SNVG GTPSTL
2451	PPFTITHPVE	TSSALLAWSR	PVRTFSTMVS	TDASGENPT	SSNSVVT SVP

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
2501	APGTWASVGS	TTDLPAMGFL	KTSPAGEAHS	LLASTIEPAT	AFTPHLSAAV
2551	VTGSSATSEA	SLLTTSSESKA	IHSSPQTPTT	PTSGANWETS	ATPESLLVVT
2601	ETSDTTLTISK	ILVTDITLFS	TVSTPPSKFP	STGTLSGASF	PTLLPDTPAI
2651	PLTATEPTSS	LATSFDSTPL	VTIASDSLGT	VPETTLTMSE	TSNGDALVLK
2701	TVSNPDRSIP	GITIQGVTES	PLHPSSTSPS	KIVAPRNTTY	EGSITVALST
2751	LPAGTTGSLV	FSQSSENSET	TALVDSSAGL	ERASVMPLTT	GSQGMASGG
2801	IRSGSTHSTG	TKTFSSLPLT	MNPGEVTAMS	EITTNRLTAT	QSTAPKGIPV
2851	KPTSAESGLL	TPVSASSSPS	KAFASLTAP	PSTWGIPQST	LTFEFSEVPS
2901	LDTKSASLPT	PGQSLNTIPD	SDASTASSSL	SKSPEKNPRA	RMMTSTKAIS
2951	ASSFQSTGFT	ETPEGSASPS	MAGHEPRVPT	SGTGDPRIAS	ESMSYPDPK
3001	ASSAMTSTSL	ASKLTTLFST	GQAARSGSSS	SPISLSTEKE	TSFLSPTAST
3051	SRKTSFLGFP	SMARQPNILV	HLQTSALTLS	PTSTLNMSQE	EPELTSSQT
3101	IAEEEGTTAE	TQTLTFTPSE	TPTSLLEPVSS	PTEPTARRKS	SPETWASSIS
3151	VPAKTSLVET	TDGTLVTTIK	MSSQAAQNS	TWPAPAEETG	TSPAGTSPGS
3201	PEVSTTLKIM	SSKEPSISPE	IRSTVRNSPA	KTPETIVPME	TTVEPVTLOS
3251	TALGSGSTSI	SHLPTGTTSP	TKSPTENMLA	TERVSLSPSP	PEAWTNLYSG
3301	TPGGTRQSLA	TMSSVSLESP	TARSITGTGQ	QSSPELVSKT	TGMEFSMWHG
3351	STGGTTGDTH	VSLSTSSNIL	EDPVTSPNSV	SSLTDKSKHK	TETWVSTTAI
3401	PSTVLNNKIM	AAEQQTSRSV	DEAYSSSTSSW	SDQTSGSDIT	LGASPDVTNT
3451	LYITSTAQTT	SLVSLPSGDQ	GITSLTNPSG	GKTSSASSVT	SPSIGLETLR
3501	ANVSAVKSDI	APTAGHLSQT	SSPAEVSILD	VTTAPTGIS	TTITTMGTNS
3551	ISTTTPNPEV	GMSTMDSTPA	TERRTTSTEH	PSTWSSTAAS	DSWTVTDMTS
3601	NLKVARSPGT	ISTMHTTSFL	ASSTELDSMS	TPHGRITVIG	TSLVTPSSDA
3651	SAVKTETSTS	ERTLSPSDTT	ASTPISTFSR	VQRMSISVPD	ILSTSWTPSS
3701	TEAEDVPVSM	VPTDHASTKT	DPNTPLSTFL	FDSLSTLDWD	TGRSLSSATA

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
3751	TTSAPQGATT	PQELTLETMI	SPATSQLPFS	IGHITSAVTP	AAMARSSGVT
3801	FSRPDPTSKK	AEQTSTQLPT	TTSAHPGQVP	RSAATTLDVI	PHTAKTPDAT
3851	FQRQGQTALT	TEARATSDSW	NEKEKSTPSA	PWITEMMNSV	SEDTIKEVTS
3901	SSSVLKDPEY	AGHKLGIWDD	FIPKFGKAAH	MRELPLLSP	QDKEAIHPST
3951	NTVETTGWVT	SSEHASHSTI	PAHSASSKLT	SPVTTSTRE	QAIVSMSTTT
4001	WPESTRARTE	PNSFLTIELR	DVSPYMDTSS	TTQTSIISSP	GSTAITKGHR
4051	TEITSYKRIS	SSFLAQSMRS	SDSPSEAITR	LSNFPAMTES	GGMILAMQTS
4101	PPGATSISAP	TLDTSATASW	TGTPLATTQR	FTYSEKTTLF	SKGREDTSQP
4151	SPPCVEETSS	SSSVVPIHAT	TSPSNILLTS	QGHSPSSTPP	VTSVFLSETS
4201	GLGKTTDMSR	ISLEPGTSLP	PNLSSTAGEA	LSTYEASRDT	KAIHHSADTA
4251	VINMEATSSE	YSPIPGHTKP	SKATSPLVTS	HIMGDITSST	SVFGSSETTE
4301	IETVSSVNQG	LQERSTSQVA	SSATETSTVI	THVSSGDATT	HVTKTQATFS
4351	SGTSSISPHQ	FITSTNTFTD	VSTNPSTSLI	MTESSGVTIT	TQTGPTGAAT
4401	QGPYLLDTST	MPYLTETPLA	VTPDFMQSEK	TTLISKGPKD	VTWTSPPSVA
4451	ETSYPSLTP	FLVTTIPPAT	STLQGQHTSS	PVSATSVLTS	GLVKTTDMLN
4501	TSMEPVTNSP	QNLNNPSNEI	LATLAATTDI	ETIHPSINKA	VTNMGTASSA
4551	HVLHSTLPVS	SEPSTATSPM	VPASSMGDAL	ASISIPGSET	TDIEGEPTSS
4601	LTAGRKENST	LQEMNSTTES	NIILSNVSVG	AITEATKMEV	PSFDATEIPT
4651	PAQSTKFPDI	FSVASSRLSN	SPPMTISTHM	TTTQTGSSGA	TSKIPLALDT
4701	STLETSAGTP	SVVTEGFAHS	KITTAMNDV	KDVSQTNPPF	QDEASSPSSQ
4751	APVLVTTLPS	SVAFTPWHS	TSSPVMSSV	LTSSLVKTAG	KVDTSLTETV
4801	SSPQMSNTL	DDISVTSAA	TDIETHPSI	NTVVTVNGTT	GSAFESHSTV
4851	SAYPEPSKVT	SPNVTTSTME	DTTISRIPK	SSKTTRTETE	TTSSLTPKLR
4901	ETSIQEITS	STETSTVPYK	ELTGATTEVS	RTDVTSSSS	SFPGPDQSTV
4951	SLDISTETNT	RLSTSPIMTE	SABITITTQT	GPHGATSQDT	FTMDPSNTTP

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
5001	QAGIHSAMTH	GFSQLDVTTL	MSRIPQDVSW	TSPPSVDKTS	SPSSFLSSPA
5051	MTTPSLISST	LPEDKLSSPM	TSLLTSGLVK	ITDILRTRLE	PVTSSLPNFS
5101	STSDKILATS	KDSKDTKEIF	PSINTEETNV	KANNSGHESH	SPALADSETP
5151	KATTQMVITT	TVGDPAPSTS	MPVHGSSETT	NIKREPTYFL	TPRLRETSTS
5201	QESSFPTDTS	FLLSKVPTGT	ITEVSSTGVI	SSSKISTPDH	DKSTVPPDTF
5251	TGEIPRVFTS	SIKTKSAEMT	ITTQASPPES	ASHSTLPLDT	STTLSQGGTH
5301	STVSQGFYPS	EVTTLMGMP	GNVSWMTTPP	VEETSSVSSL	MSSPAMTSPS
5351	PVSSTSPQSI	PSSPLPVTL	PTSVLVTTTD	VLGTTSPESV	TSSPPNLSSI
5401	THERPATYKD	TAHTEAAMHH	STNTAVTNVG	TSGSGHKSQS	SVLADSETSK
5451	ATPLMSTAST	LGDTSVSTST	PNISQTNQIQ	TEPTASLSPR	LRESSTSEKT
5501	SSTTETNTAF	SYVPTGAIQ	ASRTEISSR	TSISDLDRST	IAPDISTGMI
5551	TRLFTSPIMT	KSAEMTVTTQ	TTTPGATSQG	ILPWDSTTL	FQGGTHSTVS
5601	QGFPHSEITT	LRSRTPGDVS	WMTTPPVEET	SSGFSLMSPS	MTSPSPVSST
5651	SPESIPSSPL	PVTALLTSVL	VTTTNVLGTT	SPEPVTSSPP	NLSSPTQERL
5701	TTYKDTAHE	AMHASMHTNT	AVANVGTSIS	GHEQSSVPA	DSHTSKATSP
5751	MGITFAMGDT	SVYTSTPAFF	ETRIQSESTS	SLIPGLRDTR	TSEEINTVTE
5801	TSTVLSEVPT	TTTTEVSRTE	VITSSRTTIS	GPDHSMSPY	ISTETITRLS
5851	TFPFVTGSTE	MAITNQTGPI	GTISQATLTL	DTSSASWEG	THSPVTQRFP
5901	HSEETTTMSR	STKGVSWQSP	PSVEETSSPS	SPVPLPAITS	HSSLYSAVSG
5951	SSPTSALPVT	SLLTSGRRKT	IDMLDTHSEL	VTSSLPSASS	FSGEILTSEA
6001	STNTETIHFS	ENTAETNMGT	TNSMHLHSS	VSIHSQPSGH	TPPKVTGSMM
6051	EDAIVSTSTP	GSPETKNVDR	DSTSPLTPEL	KEDSTALVMN	STTESNTVFS
6101	SVSLDAATEV	SRAEVYYDP	TFMPASQST	KSPDISPEAS	SSHSNSPPLT
6151	ISTHKTIATQ	TGPGSVTSLG	QLTLDTSTIA	TSAGTPSART	QDFVDSETTS
6201	VMNNDLNDVL	KTSPFSAEEA	NSLSSQAPLL	VTTSPSPVTS	TLQEHSTSSL

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
6251	VSVTSVPTPT	LAKITDMDTN	LEPVTRSPQN	LRNTLATSEA	TTDTHTMHPS
6301	INTAMANVGT	TSSPNEFYFT	VSPDSDPYKA	TSVVITSTS	GDSIVSTSM
6351	RSSAMKKIES	ETTFSLIFRL	RETSTSQKIG	SSSDTSTVFD	KAFTAAATTEV
6401	SRTELTSSSR	TSIQGTEKPT	MSPDTSTRSV	TMLSTFAGLT	KSEERTIATQ
6451	TGPHRATSQG	TLTWDTSITT	SQAGTHSMT	HGFSQLDLST	LTSRVPEYIS
6501	GTSPPSVEKT	SSSSLLSLP	AITSPSPVPT	TLPESRPSSP	VHLTSLPTSG
6551	LVKTTDMLAS	VASLPPNLGS	TSHKIPTTSE	DIKDTEKMYP	STNIAVTNVG
6601	TTTSEKESYS	SVPAYSEPPK	VTSPMVTSE	IRDTIVSTSM	PGSSEITRIE
6651	MESTFSLAHG	LKGTSTSQDP	IVSTEKSAVL	HKLTGATET	SRTEVASSRR
6701	TSIPGPDHST	ESPDISTEVI	PSLPISLGIT	ESSNMTIITR	TGPPLGSTSQ
6751	GTFTLDTPTT	SSRAGTHSMA	TQEFPHSEMT	TVMNKDPEIL	SWTIPPSIEK
6801	TSFSSSLMPS	PAMTSPPVSS	TLPKTIHTTP	SPMTSLLTPS	LVMTTDTLGT
6851	SPEPTTSSPP	NLSSTSHVIL	TTDEDTTAE	AMHPSTSTAA	TNVETTCSGH
6901	GSQSSVLTD	EKTATAPMD	TTSTMGHSTV	STMSVSSET	TKIKRESTYS
6951	LTPGLRETSI	SQNASFSTD	SIVLSEVPTG	TAEVSRTEV	TSSGRTSIPG
7001	PSQSTVLPEI	STRMTLRLFA	SPTMTESAEM	TIPTQTGPSG	STSQDTLTD
7051	TSTTKSQAKT	HSTLTQRFPH	SEMTTLMRSG	PGDMSWQSSP	SLENPSSLPS
7101	LLSLPATTSP	PPISSTLPVT	ISSSPLPVT	LLTSSPVTTT	DMLHTSPELV
7151	TSSPPKLSHT	SDERLTGKD	TTNTEAVHPS	TNTAASNVEI	PSFGHESPSS
7201	ALADSETSKA	TSPMFITSTQ	EDTTVAISTP	HFLETSRIQK	ESISLSPKL
7251	RETGSSVETS	SAIETSAVLS	EVSIGATTEI	SRTEVTSSSR	TSISGSAEST
7301	MLPEISTTRK	IIKFPTSPIL	AESSEMTIKT	QTSPPGSTSE	STFTLDTSTT
7351	PSLVITHSTM	TQRLPHSEIT	TLVSRGAGDV	PRPSSLPVEE	TSPSSQLSL
7401	SAMISPPVVS	STLPASSHSS	SASVTSPLTP	GQVKTTEVLD	ASAEPETSSP
7451	PSLSSTSVEI	LATSEVTTDT	EKIHPFPNTA	VTKVGTSSSG	HESPSSVLDP

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
7501	SETTKATSAM	GTISIMGDTs	VSTLTpALSN	TRKIQSEPAS	SLTTRLRETS
7551	TSEETSLATE	ANTVLskVST	GATTEVSRTE	AISFSRTSMS	GPEQSTMSQD
7601	ISIGTIpRIS	ASSVLTESAK	MTITTQTGPS	ESTLESTLNL	NTATTPSWVE
7651	THSIVIQGFp	HPemTTSMGR	GPGGVSWPSP	PFVKETSPPS	SPLSLPAVTS
7701	PHpVSTTFLA	HIPPSPLPVT	SLLTSGPATT	TDILGTSTEP	GTSSSSSLST
7751	TSHERLTtYK	DTAHTeAVHP	STNTGGTNVA	TTSSGYKSQS	SVLADSSPMC
7801	TTSTMGDTSV	LTSTPAFLET	RRIQTElASS	LTPGLRESSG	SEGTSsGtKM
7851	STVLskVPTG	ATTEISKEDV	TSIPGPAQST	ISPDTSTRTV	SWFSTSPVMT
7901	ESAEITMnTH	TSPLGATTQg	TSTLDTSSTT	SLTMTHSTIS	QGFSHSQMST
7951	LMRRGPEDVS	WMSpPLeKT	RPSFSLMSSP	ATTSPSPVSS	TLpESISSSP
8001	LPVTSLLTSG	LAKTTDMLHK	SSEPVTNSPA	NLSSTSVEIL	ATSEVTTDTE
8051	KTHPSSNRTV	TDVGTSSSGH	ESTSFVLADS	QTSKVTSPMV	ITSTMEDTSV
8101	STSTPGFFET	SRIQTEPTSS	LTLGLRKtSS	SEGTSLATEM	STVLsgVPTG
8151	ATAEVSRTEV	TSSSRtSISG	FAQLTVSPET	STETITRLPT	SSIMTESAEM
8201	MIKTQTDPPG	STPEStHTVD	ISTTPNwVET	HSTVTQRFSH	SEMTTLVSRs
8251	PGDMLWPSQS	SVEETSSASS	LLSLPATTSP	SPVSSTLVED	FPSASLPVTS
8301	LLTPGLVITT	DRMGISREPG	TSSTSNLSST	SHERLTtLED	TVDTEAMQPS
8351	THTAVTNVRT	SISGHESQSS	VLSDSETPKA	TSSMGtTYTM	GETSVSIStS
8401	DFFETSRVQI	EPTSSLTSGL	RETSSSERIS	SATEGSTVLS	EVPSGATTEV
8451	SRTEVISSRG	TMSGPDQFT	ISPDIStEAI	TRLSTSPIMT	ESAESAITIE
8501	TGSPGATSEG	TLTLDtSTTT	FWSGTHStAS	PGFSHSEMTT	LMSRTPGDVP
8551	WPSLPSVEEA	SSVSSSLSSP	AMTSTSFFSA	LPESISSSPH	PVTALLTLGP
8601	VKTTDMLRTS	SEPETSSPPN	LSSTSAEILA	TSEVTKDREK	IHPSSNTPVV
8651	NVGTVIYKHL	SPSSVLADLV	TTKPTSPMAT	TSTLGNTSVS	TSTPAFPETM
8701	MTQPTSSLTS	GLREISTSQE	TSSATERSAS	LSGMPTGATT	KVSrTEALSL

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
8751	GRTSTPGPAQ	STISPEISTE	TITRISTPLT	TTGSAEMTIT	PKTGHSGASS
8801	QGTFTLDTSS	RASWPGTHSA	ATHRSPHSGM	TTPMSRGPED	VSWPSRPSVE
8851	KTSPSSLVS	LSAVTSPSPL	YSTPSESSH	SPLRVTSLFT	PVMMKTTDML
8901	DTSLEPVTTT	PPSMNITSDE	SLATSKATME	TEAIQLSENT	AVTQMGITISA
8951	RQEFYSSYPG	LPEPSKVTSP	VVTSSTIKDI	VSTTIPASSE	ITRIEMESTS
9001	TLTPTPRETS	TSQEIHSATK	PSTVPYKALT	SATIEDSMTQ	VMSSSRGPSP
9051	DQSTMSQDIS	TEVITRLSTS	PIKAESTEMT	ITTQTGSPGA	TSRGTLTLD
9101	STTFMSGTHS	TASQGFHSQ	MTALMSRTPG	DVPWLSHPSV	EEASSASFSL
9151	SSPVMTSSSP	VSSTLPDSIH	SSSLPVTSL	TSGLVKTTTEL	LGTSSEPETS
9201	SPPNLSSTSA	EILATTEVTT	DTEKLEMTNV	VTSGYTHESP	SSVLADSVTT
9251	KATSSMGITY	PTGDTNVLTS	TPAFSDTSRI	QTKSKLSLTP	GLMETSISEE
9301	TSSATEKSTV	LSSVPTGATT	EVSRTAIAIS	SRTSIPGPAQ	STMSSDTSME
9351	TITRISTPLT	RKESTDMAIT	PKTGPSGATS	QGTFTLDSSS	TASWPGTHSA
9401	TTQRFQSVV	TTPMSRGPED	VSWPSPLSVE	KNSPPSSLVS	SSSVTSPSPL
9451	YSTPSGSSH	SPVPVTSLFT	SIMMKATDML	DASLEPETTS	APNMNITSDE
9501	SLATSKATTE	TEAIHVFENT	AASHVETTS	TEELYSSSPG	FSEPTKVISP
9551	VVTSSSIRDN	MVSTTMPGSS	GITRIEIESM	SSLTPGLRET	RTSQDITSST
9601	ETSTVLYKMS	SGATPEVSRT	EVMPSSRTSI	PGPAQSTMSL	DISDEVVTRL
9651	STSPIMTESA	EITITTQTGY	SLATSQVTLP	LGTSMTFLSG	THSTMSQGLS
9701	HSEMTNLMSR	GPESLSWTSP	RFVETTRSSS	SLTSLPLTTS	LSPVSSTLLD
9751	SSPSSPLPVT	SLILPGLVKT	TEVLDTSSEP	KTSSSPNLSS	TSVEIPATSE
9801	IMTDTEKIHP	SSNTAVAKVR	TSSSVHESHS	SVLADSETTI	TIPSMGITSA
9851	VDDTTVFTSN	PAFSETRRIP	TEPTFSLTPG	FRETSTSEET	TSITETSAVL
9901	YGVPTSATTE	VSMTEIMSSN	RTHIPDSDQS	TMSPDIIITEV	ITRLSSSSMM
9951	SESTQMTITT	QKSSPGATAQ	STLTLATTTA	PLARTHSTVP	PRFLHSEMTT

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
10001	LMSRSPENPS	WKSSPFVEKT	SSSSLLSLP	VTTSPSVSST	LPQSIPSSSF
10051	SVTSLLTSGM	VKTDTSTEP	GTSLSPNLG	TSVEILAASE	VTTDETEIHP
10101	SSSMAVTNVG	TTSSGHELYS	SVSIHSEPSK	ATYPVGTPSS	MAETSISTSM
10151	PANFETTGF	AEPFSLTSG	FRKTNMSLD	SSVTPTNTPS	SPGSTHLLQS
10201	SKTDFETSSAK	TSSPDWPPAS	QYTEIPVDII	TPFNASPSIT	ESTGITSFPE
10251	SRFTMSVTES	THHLSTDLLP	SAETISTGTV	MPSLSEAMTS	FATTGVPRAI
10301	SGSGSPFSRT	ESGPGDATLS	TIAESLPSST	PVPFSSSTFT	TTDSSTIPAL
10351	HEITSSSATP	YRVDTSLGTE	SSTTEGRLVM	VSTLDTSSQP	GRTSSSTPILD
10401	TRMTESVELG	TVTSAYQVPS	LSTRLTRTDG	IMEHITKIPN	EAAHRTGIRP
10451	VKGPQTSTSP	ASPKGLHTGG	TKRMETTTTA	LKTTTTALKT	TSRATLTTSV
10501	YTPTLGLTLP	LNASRQMAST	ILTEMMITTP	YVFPDVPETT	SSLATSLGAE
10551	TSTALPRTTP	SVLNRESETT	ASLVSRSGAE	RSPVIQTLDV	SSSEPDTTAS
10601	WVIHPAETIP	TVSKTTPNFF	HSELDTVSST	ATSHGADVSS	AIPTNISPS
10651	LDALTPLVTI	SGTDTSTTFP	TLTKSPHETE	TRTTWLTHPA	ETSSTIPRTI
10701	PNFSHHESDA	TPSIATSPGA	ETSSAIPIMT	VSPGAEDLVT	SQVTSSGTDR
10751	NMTIPTLTLS	PGEPKTIASL	VTHPEAQTS	AIPTSTISPA	VSRLVTSMT
10801	SLAAKTSTTN	RALTNSPGEP	ATTVSLVTHP	AQTSPTVPWT	TSIFFHKS
10851	TTPSMTTSHG	AESSAVPTP	TVSTEVPGVV	TPLVTSSRAV	ISTTIPILTL
10901	SPGEPETTPS	MATSHGEEAS	SAIPTPTVSP	GVPGVVTSLV	TSSRAVTSTT
10951	IPILTFSLGE	PETTPSMATS	HGTEAGSAVP	TVLPEVPGMV	TSLVASSRAV
11001	TSTTLPTLTL	SPGEPETTPS	MATSHGAEAS	STVPTVSPEV	PGVVTSLVTS
11051	SSGVNSTSIP	TLILSPGELE	TTPSMATSHG	AEASSAVPTP	TVSPGVSGVV
11101	TPLVTSSRAV	TSTTIPILTL	SSSEPETTPS	MATSHGVEAS	SAVLTVSPEV
11151	PGMVTSLVTS	SRAVTSTTIP	TLTSSDEPE	TTTSLVTHSE	AKMISAIPTL
11201	AVSPTVQGLV	TSLVTSSGSE	TSAFSNLTVA	SSQPETIDSW	VAHPGTEASS

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
11251	VVPTLTVSTG	EPFTNISLVT	HPAESSSTLP	RTTSRFSHSE	LDTMPSTVTS
11301	PEAESSAIS	TTISPGIPGV	LTSLVTSAGR	DISATFPTVP	ESPHESEATA
11351	SWVTHPAVTS	TTVPRTTPNY	SHSEPDTTPS	IATSPGAEAT	SDFPTITVSP
11401	DVPDMVTSQV	TSSGTDTSIT	IPTLTLSAGE	PETTTSFITY	SEHTSSAIP
11451	TLPVSPGASK	MLTSLVISSG	TDSTTTFPTL	TETPYEPETT	AIQLIHPAET
11501	NTMVPRTTPK	FSHKSDDTL	PVAITSPGPE	ASSAVSTTTI	SPDMSDLVTS
11551	LVPSSGTDTS	TTFPTLSETP	YEPETTATWL	THPAETSTTV	SGTIPNFSHR
11601	GSDTAPSMVT	SPGVDTRSGV	PTTIPPSIP	GVVTSQVTSS	ATDTSTAAPT
11651	LTPSPGEPET	TASSATHPGT	QTGFTVPIRT	VPSSEPDTMA	SWVTHPPQTS
11701	TPVSRTTSSF	SHSSPDATPV	MATSPRTEAS	SAVLTTISPG	APEMVTSQIT
11751	SSGAATSTTV	PTLTHSPGMP	ETTALLSTHP	RTETSKTFPA	STVFPQVSET
11801	TASLTIRPGA	ETSTALPTQT	TSSLFTLLVT	GTSRVDLSPT	ASPGVSAKTA
11851	PLSTHPGTET	STMIPTSTLS	LGLLETTGLL	ATSSSAETST	STLTTLTVSPA
11901	VSGLSSASIT	TDKPQTVTSW	NTETSPSVTS	VGPPEFSRTV	TGTTMTLIPS
11951	EMPTPPKTSH	GEGVSPTTIL	RTTMVEATNL	ATTGSSPTVA	KTTTTFNTLA
12001	GSLFTPLTTP	GMSTLASESV	TSRTSYNHR	WISTTSSYNR	RYWTPATSTP
12051	VTSTFSPGIS	TSSIPSSTAA	TVPFMVPFTL	NFTITNLQYE	EDMRHPGSRK
12101	FNATERELQG	LLKPLFRNSS	LEYLYSGCRL	ASLRPEKDSS	AMAVDAICTH
12151	RDPEDLGLD	RERLYWELSN	LTNGIQELGP	YTLDRNSLYV	NGFTHRSSMP
12201	TTSTPGTSTV	DVGTSCTPSS	SPSPTAAGPL	LMPFTLNFTI	TNLQYEEDMR
12251	RTGSRKFNTM	ESVLQGLLKP	LFKNTSVGPL	YSGCRLTLR	PEKDGAATGV
12301	DAICTHRLDP	KSPGLNREQ	YWELSKLTND	IEELGPYTL	RNSLYVNGFT
12351	HQSSVSTTST	PGTSTVDLRT	SGTPSSLSSP	TIMAAGPLL	PFTLNFTITN
12401	LQYGEDMGHP	GSRKFNTTER	VLQGLLGPIF	KNTSVGPLY	GCRLTSLRSE
12451	KDGAATGVDA	ICIHHLDPKS	PGLNRERLYW	ELSQLTNGIK	ELGPYTLDRN

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
12501	SLYVNGFTHR	TSVPTSSTPG	TSTVDLGTSG	TPFSLPSPAT	AGPLLVLFTL
12551	NFTITNLKYE	EDMHRPGSRK	FNTTERVLQT	LLGPMFKNTS	VGLLYSGCRL
12601	TLLRSEKDGA	ATGVDAICTH	RLDPKSPGLD	REQLYWELSQ	LTNGIKELGP
12651	YTLDNRNSLYV	NGFTHWIPVP	TSSTPGTSTV	DLGSGTPSSL	PSPTAAGPLL
12701	VPFTLNFTIT	NLQYEEDMHH	PGSRKFNTTE	RVLQGLLGPM	FKNTSVGLLY
12751	SGCRLTLLRS	EKDGAATGVD	AICTHRLDPK	SPGVDREQLY	WELSQTNGI
12801	KELGPYTLDR	NSLYVNGFTH	QTSAPNTSTP	GTSTVDLGTS	GTPSSLPSPT
12851	SAGPLLVPFT	LNFTITNLQY	EEDMRHPSGR	KFNTTERVLQ	GLLKPLFKST
12901	SVGPLYSGCR	LTLRSEKDG	AATGVDAICT	HRLDPKSPGV	DREQLYWELS
12951	QLTNGIKELG	PYTLDRNSLY	VNGFTHQ TSA	PNTSTPGTST	VDLGTSGTPS
13001	SLPSPTSAGP	LLVPFTLNFT	ITNLQYEEDM	HHPGSRKFNT	TERVLQGLLG
13051	PMFKNTSVGL	LYSGCRLTLL	RPEKNGAATG	MDAICSHRLD	PKSPGLNREQ
13101	LYWELSQTTH	GIKELGPYTL	DRNSLYVNGF	THRSSVAPTS	TPGTSTVDLG
13151	TSGTPSSLPS	PTTAVPLLVP	FTLNFTITNL	QYGEDMRHPG	SRKFNTTERV
13201	LQGLLGPLFK	NSSVGPLYSG	CRLISLRSEK	LGAATCVD AI	CTHHLNPQSP
13251	GLDREQLYWQ	LSQMTNGIKE	LGPYTLDRNS	LYVNGFTHRS	SGLTTSTPWT
13301	STVDLGTSGT	PSPVPSPTTA	GPLLVPFTLN	FTITNLQYEE	DMHRPGSRKF
13351	NATERVLQGL	LSPIFKNSSV	GPLYSGCRLT	SLRPEKDGA	TGMDAVCLYH
13401	PNPKRPGLDR	EQLYWELSQT	THNITELGPY	SLDRDSLYVN	GFTHQNSVPT
13451	TSTPGTSTVY	WATTGTPSSF	PGHTEPGPLL	IPFTFNFTIT	NLHYEENMQH
13501	PGSRKFNTTE	RVLQGLLKPL	FKNTSVGPLY	SGCRLTSLRP	EKDGAATGMD
13551	AVCLYHPNPK	RPGLDREQLY	CELSQLTHNI	TELGPYSLDR	DSLYVNGFTH
13601	QNSVPTTSTP	GTSTVYWATT	GTPSSFPGHT	EPGPLLIPFT	FNFTITNLHY
13651	EENMQHPGSR	KFNTTERVLQ	GLLKPLFKNT	SVGPLYSGCR	LTLRPEKHE
13701	AATGVDTICT	HRVDPIGPGL	DRERLYWELS	QLTNSITELG	PYTLDRDSLY

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
13751	VNGFNPRSSV	PTTSTPGTST	VHLATSGTPS	SLPGHTAPVP	LLIPFTLNFT
13801	ITNLHYEENM	QHPGSRKFNT	TERVLQGLLK	PLFKNTSVGP	LYSGCRLTLL
13851	RPEKHEAATG	VDTICTHRVD	PIGPGLDREX	LYWELSXLTX	XIXELGPYXL
13901	DRXSLYVNGF	XXXXXXXXTS	TPGTSXVXLX	TSGTPXXXPX	XTSAGPLLVP
13951	FTLNFTITNL	QYEEDMHHPG	SRKFNTTERV	LQGLLGPMFK	NTSVGLLYSG
14001	CRLTLLRPEK	NGAATGMDAI	CSHRLDPKSP	GLDREQLYWE	LSQLTHGIKE
14051	LGPYTLDNRN	LYVNGFTHRS	SVAPTSTPGT	STVDLGTSST	PSSLPSPTTA
14101	VPLLVPFTLN	FTITNLQYGE	DMRHPGSRKF	NTTERVLQGL	LGPLFKNSSV
14151	GPLYSGCRLI	SLRSEKDGA	TGVDAICTHH	LNQSPGLDR	EQLYWQLSQM
14201	TNGIKELGPY	TLDNRNLYVN	GFTHRSSGLT	TSTPWTSTVD	LGTSSTPSPV
14251	PSPTTAGPLL	VPFTLNFTIT	NLQYEEDMHR	PGSRKFNATE	RVLQGLLSPI
14301	FKNSSVGPLY	SGCRLTSLRP	EKDGAATGMD	AVCLYHPNPK	RPGLDREQLY
14351	WELSQLTHNI	TELGPYSLDR	DSLYVNGFTH	QSSMTTTRTP	DTSTMHLATS
14401	RTPASLSGPT	TASPLLVLFT	INCTITNLQY	EEDMRRTGSR	KFNTMESVLQ
14451	GLLKPLFKNT	SVGPLYSGCR	LTLRPPKDG	AATGVDAICT	HRLLDPKSPGL
14501	NREQLYWELS	KLNDIEELG	PYTLDNRNLY	VNGFTHQSSV	STTSTPGTST
14551	VDLRTSGTPS	SLSSPTIMXX	XPLLXPFTLN	FTITNLXYEE	MXXPGRSRKF
14601	NTTERVLQGL	LRPLFKNTSV	SSLYSGCRLT	LLRPEKDGA	TRVDAACTYR
14651	PDPKSPGLDR	EQLYWELSQL	THSITELGPY	TLDNRNLYVN	GFNPRSSVPT
14701	TSTPGTSTVH	LATSGTPSSL	PGHTXXXPLL	XPFTLNFTIT	NLXYEEXMXX
14751	PGSRKFNTTE	RVLQGLLKPL	FRNSSLEYLY	SGCRLASLRP	EKDSSAMAVD
14801	AICTHRPDPE	DLGLDRERLY	WELSNLTNGI	QELGPYTLDNR	NLYVNGFTH
14851	RSSFLTSTP	WTSTVDLGTS	GTPSPVPSPT	TAGPLLVPFT	LNFTITNLQY
14901	EEDMRPGSR	RFNTTERVLQ	GLLTPLFKNT	SVGPLYSGCR	LTLRPEKQE
14951	AATGVDTICT	HRVDPIGPGL	DRERLYWELS	QLTNSITELG	PYTLDNRDSLY

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
15001	VNGFNPWSSV	PTTSTPGTST	VHLATSGTPS	SLPGHTAPVP	LLIPFTLNFT
15051	ITDLHYEENM	QHPGSRKFNT	TERVLQGLLK	PLFKSTSVGP	LYSGCRLTLL
15101	RPEKHGAATG	VDAICTLRLD	PTGPGLDRER	LYWELSQLTN	SVTELGPYTL
15151	DRDSLYVNGF	THRSSVPTTS	IPGTSAVHLE	TSGTPASLPG	HTAPGPPLLVP
15201	FTLNFTITNL	QYEEDMRHPG	SRKFSTTERV	LQGLLKPLFK	NTSVSSSLYSG
15251	CRLTLLRPEK	DGAATRVDV	CTHRPDPKSP	GLDRERLYWK	LSQLTHGITE
15301	LGPYTLDRHS	LYVNGFTHQS	SMTTTRTPDT	STMHLATSRT	PASLSGPTTA
15351	SPLLVLFTIN	FTITNQRYEE	NMHPGSRKF	NTTERVLQGL	LRPVFKNTSV
15401	GPLYSGCRLT	LLRPKKGAA	TKVDAICTYR	PDPKSPGLDR	EQLYWELSOL
15451	THSITELGPI	TQDRDSLYVN	GFTHRSSVPT	TSIPGTSAVH	LETSGTPASL
15501	PGHTAPGPLL	VPFTLNFTIT	NLQYEEDMRH	PGSRKFNTTE	RVLQGLLKPL
15551	FKSTSVGPLY	SGCRLTLLRP	EKRGAAATGVD	TICTHRLDPL	NPGLDREQLY
15601	WELSKLTRGI	IELGPYLLDR	GSLYVNGFTH	RTSVPTTSTP	GTSTVDLGT
15651	GTPFSLPSA	XXXPLLXPFT	LNFTITNLXY	EEXMXXPGSR	KFNTTERVLQ
15701	TLLGPMFKNT	SVGLLYSGCR	LTLRSEKDG	AATGVDAICT	HRLDPKSPGV
15751	DREQLYWELS	QLTNGIKELG	PYTLDNRSLY	VNGFTHWIPV	PTSSTPGTST
15801	VDLGSGTPSL	PSSPTTAGPL	LVPFTLNFTI	TNLKYEEDMH	CPGSRKFNTT
15851	ERVLQSLG	MPKNTSVGPI	YSGCRLTLLR	SEKDGAATGV	DAICTHRLDP
15901	KSPGVDREQL	YWELSQTNG	IKELGPYTLD	RNSLYVNGFT	HQTSAPNTST
15951	PGTSTVDLGT	SGTPSSLPS	TXXXPLLXPF	TLNFTITNLX	YEEKMXXPGS
16001	RKFNTTERVL	QGLLXPXFKX	TSVGXLYSGC	RLTLRXEKX	XAATXVDXXC
16051	XXXXDPXXPG	LDREXLYWEL	SXLTXIXEL	GPYXLDXSL	YVNGFTHWIP
16101	VPTSSTPGTS	TVDLGSGTPS	SLPSPTTAGP	LLVPFTLNFT	ITNLKYEEDM
16151	HCPGSRKFNT	TERVLQSLG	PMFKNTSVGP	LYSGCRLTSL	RSEKDGAATG
16201	VDAICTHRVD	PKSPGVDREQ	LYWELSQTNG	GIKELGPYTL	DRNSLYVNGF

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
16251	THQTSAPNTS	TPGTSTVDLG	TSGTPSSLPS	PTSAGPLLVP	FTLNFTITNL
16301	QYEEDMHHPG	SRKFNTTERV	LQGLLGPMFK	NTSVGLLYSG	CRLTLLRPEK
16351	NGAATGMDAI	CTHRLDPKSP	GLDREXLYWE	LSXLTXXIXE	LGPYXLDKXS
16401	LYVNGFXXXX	XXXXTSTPGT	SKVXLXTSGT	PXXXPXXTXX	XPLLXPFTLN
16451	FTITNLXYEE	XXXXPGSRKF	NTTERVLQGL	LKPLFRNSSL	EYLYSGCRLA
16501	SLRPEKDSSA	MAVDAICTHR	PDPEGLGLDR	ERLYWELSNL	TNGIQELGPY
16551	TLDRNSLYVN	GFTHRSSMPT	TSTPGTSTVD	VGTSCTPSSS	PSPTTAGPLL
16601	IPFTLNFTIT	NLQYGEDMGH	PGSRKFNTTE	RVLQGLLGPI	FKNTSVGPLY
16651	SGCRLTSLRS	EKDGAATGVD	AICIHHLDPK	SPGLNRERLY	WELSQTNGI
16701	KELGPYTLDR	NSLYVNGFTH	RTSVPTTSTP	GTSTVDLGTS	GTPFSLPSPA
16751	TAGPLLVLFT	LNFTITNLKY	EEDMHRPGSR	KFNTTERVLQ	TLLGPMFKNT
16801	SVGLLYSGCR	LTLLRSEKDG	AATGVDAICT	HRLLDPKSPGL	DREXLYWELS
16851	XLTXIXELG	PYXLDKXSLY	VNGFXXXXXX	XTSTPGTSX	VXLXTSGTPX
16901	XXPXXTXXXP	LLXPFTLNFT	ITNLXYEEXM	XXPGSRKFNT	TERVLQGLLR
16951	PVFKNTSVGP	LYSGCRLTLL	RPKKDGAATK	VDAICTYRPD	PKSPGLDREQ
17001	LYWELSQTTH	SITELGPYTQ	DRDSLYVNGF	THRSSVPTTS	IPGTSVAHLE
17051	TTGTPSSFPG	HTEPGPLLIP	FTFNFTITNL	RYEENMQHPG	SRKFNTTERV
17101	LQGLLTPLFK	NTSVGPLYSG	CRLTLLRPEK	QEAATGVDTI	CTHRVDPIGP
17151	GLDRERLYWE	LSQLTNSITE	LGPYTLDRDS	LYVDGFNPWS	SVPTTSTPGT
17201	STVHLATSGT	PSPLPGHTAP	VPLLIPFTLN	FTITDLHYEE	NMQHPGSRKF
17251	NTTERVLQGL	LKPLFKSTSV	GPLYSGCRLT	LLRPEKHGAA	TGVDAICTLR
17301	LDPTGPGLDR	ERLYWELSQT	TNSITELGPY	TLDRDSLYVN	GFNPWSSVPT
17351	TSTPGTSTVH	LATSGTPSSL	PGHTTAGPLL	VPFTLNFTIT	NLKYEEDMHC
17401	PGSRKFNTTE	RVLQSLHGPM	FKNTSVGPLY	SGCRLTLLRS	EKDGAATGVD
17451	AICTHRLDPK	SPGLDREXLY	WELSXLTXXI	XELGPYXLDK	XSLYVNGFXX

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
17501	XXXXXX	TSTP	GTSXVXL	XTS	ĠTPXXXXPXXT XXXPLLXPFT LNFTITNLXY
17551	EEXMXX	PGSR	KFNTT	ERVLQ	GLLXPXFKXT SVGXLYSGCR LTLRLRXEKXX
17601	AATXVD	XXCX	XXXDP	XXPGL	DREXLYWELS XLTNSITELG PYTLDRDSLY
17651	VNGF	THRSSM	PTTSIP	GTSA	VHLETSGTPA SLPGHTAPGP LLVPFTLNFT
17701	ITNLQY	EEDM	RHPGSR	KFNT	TERVLQGLLK PLFKSTSVGP LYSGCRLTLL
17751	RPEKRG	AATG	VDTIC	THRLD	PLNPGLDREX LYWELSXLTX XIXELGPYXL
17801	DRXSLY	VNGF	XXXXXXXX	TS	TPGTSXVXLX TSGTPXXXXPX XTXXXPLLXP
17851	FTLNFT	ITNL	XYEEXM	XXPG	SRKFNTTERV LQGLLXPXFK XTSVGXLYSG
17901	CRLTLL	RXKEK	XXAATX	VDXX	CXXXXDPXXP GLDREXLYWE LSXLTXIXE
17951	LGPYXL	DRXS	LYVNG	FHPRS	SVPTTSTPGT STVHLATSGT PSSLPGHTAP
18001	VPLLIP	FTLN	FTITNL	HYEE	NMQHPGSRKF NTTERVLQGL LGPMFKNTSV
18051	GLLYSG	CRLT	LLRPEK	NGAA	TGMDAICSHR LDPKSPGLDR EXLYWELSXL
18101	TXXIXE	LGPY	XLDRX	SLYVN	GFXXXXXXXXXX TSTPGTSXVX LXTSGTPXXX
18151	PXXTXXX	PLL	XPFTLN	FTIT	NLXYEEXMXX PGSRKFNTE RVLQGLLXPX
18201	FKXTSV	GXLY	SGCRLT	LLRX	EKXXAATXVD XXCXXXXDPX XPGLDREXLY
18251	WELSXL	TXXI	XELGPY	XLDR	XSLYVNGFTH QNSVPTTSTP GTSTVYWATT
18301	GTPSSF	PGHT	EPGPLL	IPFT	FNFTITNLHY EENMQHPGSR KFNTTERVLQ
18351	GLLTPL	FKNT	SVGPLY	SGCR	LTLRLPEKQE AATGVDTICT HRVDPIGPGL
18401	DREXLY	WELS	XLTXIX	ELG	PYXLDRXSLY VNGFXXXXXX XXTSTPGTSX
18451	VXLXTS	GTPX	XXPXXT	XXXXP	LLXPFTLNFT ITNLXYEEXM XXPGSRKFNT
18501	TERVLQ	GLLX	PXFKXT	SVGX	LYSGCRLTLL RXEKXXAATX VDXXCXXXXD
18551	PXXPGL	DREX	LYWELS	XLTX	XIXELGPYXL DRXSLYVNGF THRSSVPTTS
18601	SPGTST	VHLA	TSGTPSS	LPG	HTAPVPLLIP FTLNFTITNL HYEENMQHPG
18651	SRKFNT	TERV	LQGLLK	PLFK	STSVGPLYSG CRLTLLRPEK HGAATGVDAI
18701	CTLRLD	PTGP	GLDREX	LYWE	LSXLTXIXE LGPYXLDRXS LYVNGFXXXXX

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
18751	XXXXTSTPGT	SXVXLXTSGT	PXXXPXXTXX	XPLLXPFTLN	FTITNLXYEE
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18851	TXVDXXCXXX	XDPPXPGLDR	EXLYWELSXL	TXXIXELGPY	XLDRXSPLYVN
18901	GFTHRTSVPT	TSTPGTSTVH	LATSGTPSSL	PGHTAPVPLL	IPFTLNFTIT
18951	NLQYEEDMHR	PGSRKFNTTE	RVLQGLLSPI	FKNSSVGPLY	SGCRLTSLRP
19001	EKDGAATGMD	AVCLYHPNPK	RPGLDREQLY	CELSQLTHNI	TELGPLYSLDR
19051	DSLYVNGFTH	QNSVPTTSTP	GTSTVYWATT	GTPSSFPGHT	XXXPLLXPFT
19101	LNFTITNLXY	EEXMXXPGSR	KFNTTERVLQ	GLLXPXFKXT	SVGXLYSGCR
19151	LTLRLXKXX	AATXVDXXCX	XXXDPXXPGL	DREXLYWELS	XLTXIXELG
19201	PYXLDRXSLY	VNGFTHWSSG	LTTSTPWTST	VDLGTSGTPS	PVPSPPTAGP
19251	LLVPFTLNFT	ITNLQYEEDM	HRPGSRKFNA	TERVLQGLLS	PIFKNTSVGP
19301	LYSGCRLTLL	RPEKQEAATG	VDTICTHRVD	PIGPGLDREX	LYWELSXLTX
19351	XIXELGPYXL	DRXSPLYVNGF	XXXXXXXXXTS	TPGTSXVXLX	TSGTPXXXPX
19401	XTXXXPLLXP	FTLNFTITNL	XYEEXMXXPG	SRKFNTTERV	LQGLLXPXFK
19451	XTSVGXLYSG	CRLTLRLXKX	XXAATXVDXX	CXXXDPXXP	GLDREXLYWE
19501	LSXLTXIXE	LGPYXLDRXS	LYVNGFTHRS	FGLTTSTPWT	STVDLGTSGT
19551	PSPVPSPTTA	GPLLVPFTLN	FTITNLQYEE	DMHRPGSRKF	NTTERVLQGL
19601	LTPLFRNTSV	SSLYSGCRLT	LLRPEKDGA	TRVDAVCTHR	PDPKSPGLDR
19651	EXLYWELSXL	TXXIXELGPY	XLDRXSPLYVN	GFXXXXXXXXX	TSTPGTSXVX
19701	LXTSGTPXXX	PXXTXXXPLL	XPFTLNFTIT	NLXYEEXMXX	PGSRKFNTTE
19751	RVLQGLLXPX	FKXTSVGXLY	SGCRLTLRLX	EKXXAATXVD	XXCXXXDPX
19801	XPGLDREXLY	WELSXLTXXI	XELGPYXLDR	XSLYVNGFTH	WIPVPTSSTP
19851	GTSTVDLGSG	TPSSLPSPTT	AGPLLVPFTL	NFTITNLQYG	EDMGHPGSRK
19901	FNTTERVLQG	LLGPIFKNTS	VGPLYSGCRL	TSLRSEKDGA	ATGVDAICIH
19951	HLPKSPGLD	REXLYWELSX	LTXIXELGP	YXLDRXSPLYV	NGFXXXXXXXX

Table 5 (continued)

Human Protein of CA125 Molecule
(SEQ ID NO: 5)

20001	XTSTPGTSXV	XLXTSGTPXX	XPXXTXXXPL	LXPFTLNFTI	TNLXYEEXMX
20051	XPGSRKFNTT	ERVLQGLLXP	XFKXTSVGXL	YSGCRLTLLR	XEKXXAATXV
20101	DXXCXXXXDP	XXPGLDREXL	YWELSXLTX	IXELGPYXLD	RXSLYVNGFT
20151	HQTFAPNTST	PGTSTVDLGT	SGTPSSLPSP	TSAGPLLVPF	TLNFTITNLQ
20201	YEEDMHHPGS	RKFNTTTERVL	QGLLGPMFKN	TSVGLLYSGC	RLTLLRPEKN
20251	GAATRVDVAVC	THRPDPKSPG	LDREXLYWEL	SXLTXIXEL	GPYXLDRXSL
20301	YVNGFXXXXX	XXXTSTPGTS	XVXLXTSGTP	XXXPXXTAPV	PLLIPFTLNF
20351	TITNLHYEEN	MQHPGSRKFN	TTERVLQGLL	RPLFKSTSVG	PLYSGCRLTL
20401	LRPEKHGAAT	GVDAICTLRL	DPTGPGLDRE	RLYWELSQLT	NSVTELGPYT
20451	LDRDSLYVNG	FTQRSSVPTT	SIPGTSAVHL	ETSGTPASLP	GHTAPGPLL
20501	PFTLNFTITN	LQYEVDMRHP	GSRKFNTTER	VLQGLLKPLF	KSTSVGPLYS
20551	GCRLTLLRPE	KRGAATGVDT	ICTHRLDPLN	PGLDREQLYW	ELSKLTRGII
20601	ELGPYLLDRG	SLYVNGFTHR	NFVPITSTPG	TSTVHLGTSE	TPSSLPRPIV
20651	PGPLLVPFTL	NFTITNLQYE	EAMRHGSRK	FNTTTERVLQ	LLRPLFKNTS
20701	IGPLYSSCRL	TLLRPEKDKA	ATRVDAICTH	HPDPQSPGLN	REQLYWELSQ
20751	LTHGITELGP	YTLDRDSLYV	DGFTHWSPIP	TTSTPGTSIV	NLGTSGIPPS
20801	LPETTXXXPL	LXPFTLNFTI	TNLXYEEXMX	XPGSRKFNTT	ERVLQGLLKP
20851	LFKSTSVGPL	YSGCRLTLLR	PEKDGVA TRV	DAICTHRPDP	KIPGLDRQQL
20901	YWELSQTLS	ITELGPYTLD	RDSLYVNGFT	QRSSVPTTST	PGTFTVQPET
20951	SETPSSLPGP	TATGPVLLPF	TLNFTITNLQ	YEEDMHRPGS	RKFNTTTERVL
21001	QGLLMPLFKN	TSVSSLYSGC	RLTLLRPEKD	GAATRVDVAVC	THRPDPKSPG
21051	LDRERLYWKL	SQLTHGITEL	GPYTLDRHSL	YVNGFTHQSS	MTTTRTPDTS
21101	TMHLATS RTP	ASLSGPTTAS	PLLVLF TINF	TITNLRYEEN	MHHPGSRKFN
21151	TTERVLQGLL	RPVFKNTSVG	PLYSGCRLTL	LRPKKDGAA T	KVDAICTYRP
21201	DPKSPGLDRE	QLYWELSQLT	HSITELGPYT	QDRDSLYNNG	FTQRSSVPTT

Table 5 (continued)

Human Protein of CA125 Molecule (SEQ ID NO: 5)					
21251	SVPGTPTVDL	GTSGTPVSKP	GPSAASPLLV	LFTLNGTITN	LRYEENMQHP
21301	GSRKFNTTER	VLQGLLRSLF	KSTSVGPLY	GCRLTLLRPE	KDGTATGVDA
21351	ICTHHPDPKS	PRLDREQLYW	ELSQLTHNIT	ELGHYALDND	SLFVNGFTHR
21401	SSVSTTSTPG	TPTVYLGA	TPASIFGPSA	ASHLLILFTL	NFTITNLRYE
21451	ENMWPGSRKF	NTTERVLQGL	LRPLFKNTSV	GPLYSGSRLT	LLRPEKDGEA
21501	TGVDAICTHR	PDPTGPGLDR	EQLYLELSQL	THSITELGPY	TLDRDSLYVN
21551	GFTHRSSVPT	TSTGVVSEEP	FTLNFTINNL	RYMADMGQPG	SLKFNITDNV
21601	MKHLLSPLFQ	RSSLGARYTG	CRVIALRSVK	NGAETRVDLL	CTYLQPLSGP
21651	GLPIKQVFHE	LSQQTHGITR	LGPYSLDKDS	LYLNGYNEPG	LDEPPTTPKP
21701	ATTFLPPLSE	ATTAMGYHLK	TLTLNFTISN	LQYSPDMGKG	SATFNSTEGV
21751	LQHLLRPLFQ	KSSMGPFYLG	CQLISLRPEK	DGAATGVDDT	CTYHPDPVGP
21801	GLDIQQLYWE	LSQLTHGVTQ	LGFYVLDRDS	LFINGYAPQN	LSIRGEYQIN
21851	FHIVNWNLSN	PDPTSSEYIT	LLRDIQDKVT	TLYKGSQ LHD	TFRFCLVTNL
21901	TMDSVLVTVK	ALFSSNLDPS	LVEQVFLDKT	LNASFHWLGS	TYQLVDIHVT
21951	EMESSVYQPT	SSSSTQH FYL	NFTITNLPYS	QDKAQPGTTN	YQRNKRNIED
22001	ALNQLFRNSS	IKSYFSDCQV	STFRSVPNRH	HTGVDSL CNF	SPLARRVDRV
22051	AIYE EFLRMT	RNGTQLQNFT	LDRSSVLVDG	YSPNRNEPLT	GNSDLPFWAV
22101	ILIGLAGLLG	LITCLICGVL	VTTRRRKKEG	EYNVQQQCPG	YYQSHLDLED
22151	LQ				

WE CLAIM

1. An isolated nucleic acid molecule encoding CA125.
2. The isolated nucleic acid molecule of claim 1 comprising the sequence of SEQ ID NO: 4.
3. The isolated nucleic acid molecule of claim 2 wherein the sequence has at least about 70% homology with SEQ ID NO: 4.
4. The isolated nucleic acid molecule of claim 2 wherein said molecule is a fragment thereof.
5. An isolated nucleic acid molecule comprising the sequence shown in SEQ ID NO: 1.
6. The isolated nucleic acid molecule of claim 5 wherein the sequence has at least about 70% homology with SEQ ID NO: 1.
7. The isolated nucleic acid molecule of claim 5 wherein said molecule is a fragment thereof.
8. An isolated nucleic acid molecule comprising the sequence shown in SEQ ID NO: 2.
9. The isolated nucleic acid molecule of claim 8 wherein the sequence has at least about 70% homology with SEQ ID NO: 2.
10. The isolated nucleic acid molecule of claim 8 wherein said molecule is a fragment thereof.
11. An isolated nucleic acid molecule comprising the sequence shown in SEQ ID NO: 3.
12. The isolated nucleic acid molecule of claim 11 wherein the sequence has at least about 70% homology with SEQ ID NO: 3.
13. The isolated nucleic acid molecule of claim 11 wherein said molecule is a fragment thereof.
14. A polypeptide with the amino acid sequence selected from the group consisting of: (a) the amino acid sequence set forth in SEQ ID NO: 5; (b) an amino acid sequence having at least 50% sequence identity to said sequence; (c) a conservative variant of an one of (a) to (b); and (d) a fragment of any one of (a) to (c).
15. A purified antibody that selectively binds to an amino acid sequence of the CA125 protein:
 - (a) wherein the amino acid sequence of the CA125 protein comprises the amino acid sequence set forth in SEQ ID NO: 5;

- (b) an amino acid sequence having at least 50% sequence identity to said sequence;
 - (c) a conservative variant of any one of (a) to (b); and
 - (d) a fragment of any one of (a) to (c).
16. The purified antibody of claim 15 wherein said sequence identity is at least 60%.
17. The purified antibody of claim 15 wherein said sequence identity is at least 70%.
18. The purified antibody of claim 15 wherein said sequence identity is at least 80%.
19. The purified antibody of claim 15 wherein said sequence identity is at least 90%.
20. A method to make a purified fragment of the CA125 polypeptide of SEQ ID NO: 5 comprising:
- (a) expressing a portion of the isolated nucleic acid molecule set out in SEQ ID NO: 4 to obtain a fragment of the CA125 molecule; and
 - (b) purifying said fragment of the CA125 molecule.

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SEQUENCE LISTING

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O'Brien, Timothy
Beard, John
Underwood, Lowell

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Interventions

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022438.43867(pct2).ST25.txt

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022438.43867(pct2).ST25.txt

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 Ala Ser Asp Ser Leu Gly Thr Val Pro Glu Thr Thr Leu Thr Met
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 2690 2695 2700
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 Gly Leu Glu Arg Ala Ser Val Met Pro Leu Thr Thr Gly Ser Gln
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 Thr Gly Thr Lys Thr Phe Ser Ser Leu Pro Leu Thr Met Asn Pro
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022438.43867(pct2).ST25.txt

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Thr Leu Pro Pro Phe Thr Ile Thr His Pro Val Glu Thr Ser Ser
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 2495 2500 2505

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Lys Ala Ile His Ser Ser Pro Gln Thr Pro Thr Thr Pro Thr Ser
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 2585 2590 2595

Val Thr Glu Thr Ser Asp Thr Thr Leu Thr Ser Lys Ile Leu Val
 2600 2605 2610

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022438.43867(pct2).ST25.txt

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 1940 1945 1950
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 1955 1960 1965
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 1970 1975 1980
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 1985 1990 1995
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 2000 2005 2010
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 2015 2020 2025
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 2090 2095 2100
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 2105 2110 2115
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 2120 2125 2130
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 1730 1735 1740
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 1865 1870 1875
 Ser Asp Thr Ser Ser Lys Ser Leu Ser Met Gly Asn Ser Thr His
 1880 1885 1890
 Thr Ser Met Thr Asp Thr Glu Lys Ser Glu Val Ser Ser Ser Ile
 1895 1900 1905

022438.43867(pct2).ST25.txt

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022438.43867(pct2).ST25.txt

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 Page 205

022438.43867(pct2).ST25.txt

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 690 695 700

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 260 265 270
 Ala Gly His Ser Arg Ile Ser Thr Ser Ala Pro Leu Ser Ser Ser Ala
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 3995 4000 4005
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Ser Asn Ile Leu Leu Thr Ser Gln Gly His Ser Pro Ser Ser Thr
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Pro Pro Val Thr Ser Val Phe Leu Ser Glu Thr Ser Gly Leu Gly
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Tyr Glu Ala Ser Arg Asp Thr Lys Ala Ile His His Ser Ala Asp
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 5255 5260 5265
 Met Thr Ile Thr Thr Gln Ala Ser Pro Pro Glu Ser Ala Ser His
 5270 5275 5280
 Ser Thr Leu Pro Leu Asp Thr Ser Thr Thr Leu Ser Gln Gly Gly
 5285 5290 5295
 Thr His Ser Thr Val Ser Gln Gly Phe Pro Tyr Ser Glu Val Thr
 5300 5305 5310
 Thr Leu Met Gly Met Gly Pro Gly Asn Val Ser Trp Met Thr Thr
 5315 5320 5325
 Pro Pro Val Glu Glu Thr Ser Ser Val Ser Ser Leu Met Ser Ser
 5330 5335 5340
 Pro Ala Met Thr Ser Pro Ser Pro Val Ser Ser Thr Ser Pro Gln
 5345 5350 5355
 Ser Ile Pro Ser Ser Pro Leu Pro Val Thr Ala Leu Pro Thr Ser
 5360 5365 5370
 Val Leu Val Thr Thr Thr Asp Val Leu Gly Thr Thr Ser Pro Glu
 5375 5380 5385
 Ser Val Thr Ser Ser Pro Pro Asn Leu Ser Ser Ile Thr His Glu
 5390 5395 5400
 Arg Pro Ala Thr Tyr Lys Asp Thr Ala His Thr Glu Ala Ala Met
 5405 5410 5415
 His His Ser Thr Asn Thr Ala Val Thr Asn Val Gly Thr Ser Gly
 5420 5425 5430
 Ser Gly His Lys Ser Gln Ser Ser Val Leu Ala Asp Ser Glu Thr
 5435 5440 5445

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Ser Lys Ala Thr Pro Leu Met Ser Thr Ala Ser Thr Leu Gly Asp
 5450 5455 5460
 Thr Ser Val Ser Thr Ser Thr Pro Asn Ile Ser Gln Thr Asn Gln
 5465 5470 5475
 Ile Gln Thr Glu Pro Thr Ala Ser Leu Ser Pro Arg Leu Arg Glu
 5480 5485 5490
 Ser Ser Thr Ser Glu Lys Thr Ser Ser Thr Thr Glu Thr Asn Thr
 5495 5500 5505
 Ala Phe Ser Tyr Val Pro Thr Gly Ala Ile Thr Gln Ala Ser Arg
 5510 5515 5520
 Thr Glu Ile Ser Ser Ser Arg Thr Ser Ile Ser Asp Leu Asp Arg
 5525 5530 5535
 Ser Thr Ile Ala Pro Asp Ile Ser Thr Gly Met Ile Thr Arg Leu
 5540 5545 5550
 Phe Thr Ser Pro Ile Met Thr Lys Ser Ala Glu Met Thr Val Thr
 5555 5560 5565
 Thr Gln Thr Thr Thr Pro Gly Ala Thr Ser Gln Gly Ile Leu Pro
 5570 5575 5580
 Trp Asp Thr Ser Thr Thr Leu Phe Gln Gly Gly Thr His Ser Thr
 5585 5590 5595
 Val Ser Gln Gly Phe Pro His Ser Glu Ile Thr Thr Leu Arg Ser
 5600 5605 5610
 Arg Thr Pro Gly Asp Val Ser Trp Met Thr Thr Pro Pro Val Glu
 5615 5620 5625
 Glu Thr Ser Ser Gly Phe Ser Leu Met Ser Pro Ser Met Thr Ser
 5630 5635 5640
 Pro Ser Pro Val Ser Ser Thr Ser Pro Glu Ser Ile Pro Ser Ser
 5645 5650 5655
 Pro Leu Pro Val Thr Ala Leu Leu Thr Ser Val Leu Val Thr Thr
 5660 5665 5670
 Thr Asn Val Leu Gly Thr Thr Ser Pro Glu Pro Val Thr Ser Ser
 5675 5680 5685

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Pro Pro Asn Leu Ser Ser Pro Thr Gln Glu Arg Leu Thr Thr Tyr
 5690 5695 5700
 Lys Asp Thr Ala His Thr Glu Ala Met His Ala Ser Met His Thr
 5705 5710 5715
 Asn Thr Ala Val Ala Asn Val Gly Thr Ser Ile Ser Gly His Glu
 5720 5725 5730
 Ser Gln Ser Ser Val Pro Ala Asp Ser His Thr Ser Lys Ala Thr
 5735 5740 5745
 Ser Pro Met Gly Ile Thr Phe Ala Met Gly Asp Thr Ser Val Tyr
 5750 5755 5760
 Thr Ser Thr Pro Ala Phe Phe Glu Thr Arg Ile Gln Ser Glu Ser
 5765 5770 5775
 Thr Ser Ser Leu Ile Pro Gly Leu Arg Asp Thr Arg Thr Ser Glu
 5780 5785 5790
 Glu Ile Asn Thr Val Thr Glu Thr Ser Thr Val Leu Ser Glu Val
 5795 5800 5805
 Pro Thr Thr Thr Thr Thr Glu Val Ser Arg Thr Glu Val Ile Thr
 5810 5815 5820
 Ser Ser Arg Thr Thr Ile Ser Gly Pro Asp His Ser Lys Met Ser
 5825 5830 5835
 Pro Tyr Ile Ser Thr Glu Thr Ile Thr Arg Leu Ser Thr Phe Pro
 5840 5845 5850
 Phe Val Thr Gly Ser Thr Glu Met Ala Ile Thr Asn Gln Thr Gly
 5855 5860 5865
 Pro Ile Gly Thr Ile Ser Gln Ala Thr Leu Thr Leu Asp Thr Ser
 5870 5875 5880
 Ser Thr Ala Ser Trp Glu Gly Thr His Ser Pro Val Thr Gln Arg
 5885 5890 5895
 Phe Pro His Ser Glu Glu Thr Thr Thr Met Ser Arg Ser Thr Lys
 5900 5905 5910
 Gly Val Ser Trp Gln Ser Pro Pro Ser Val Glu Glu Thr Ser Ser
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5915 5920 5925
 Pro Ser Ser Pro Val Pro Leu Pro Ala Ile Thr Ser His Ser Ser
 5930 5935 5940
 Leu Tyr Ser Ala Val Ser Gly Ser Ser Pro Thr Ser Ala Leu Pro
 5945 5950 5955
 Val Thr Ser Leu Leu Thr Ser Gly Arg Arg Lys Thr Ile Asp Met
 5960 5965 5970
 Leu Asp Thr His Ser Glu Leu Val Thr Ser Ser Leu Pro Ser Ala
 5975 5980 5985
 Ser Ser Phe Ser Gly Glu Ile Leu Thr Ser Glu Ala Ser Thr Asn
 5990 5995 6000
 Thr Glu Thr Ile His Phe Ser Glu Asn Thr Ala Glu Thr Asn Met
 6005 6010 6015
 Gly Thr Thr Asn Ser Met His Lys Leu His Ser Ser Val Ser Ile
 6020 6025 6030
 His Ser Gln Pro Ser Gly His Thr Pro Pro Lys Val Thr Gly Ser
 6035 6040 6045
 Met Met Glu Asp Ala Ile Val Ser Thr Ser Thr Pro Gly Ser Pro
 6050 6055 6060
 Glu Thr Lys Asn Val Asp Arg Asp Ser Thr Ser Pro Leu Thr Pro
 6065 6070 6075
 Glu Leu Lys Glu Asp Ser Thr Ala Leu Val Met Asn Ser Thr Thr
 6080 6085 6090
 Glu Ser Asn Thr Val Phe Ser Ser Val Ser Leu Asp Ala Ala Thr
 6095 6100 6105
 Glu Val Ser Arg Ala Glu Val Thr Tyr Tyr Asp Pro Thr Phe Met
 6110 6115 6120
 Pro Ala Ser Ala Gln Ser Thr Lys Ser Pro Asp Ile Ser Pro Glu
 6125 6130 6135
 Ala Ser Ser Ser His Ser Asn Ser Pro Pro Leu Thr Ile Ser Thr
 6140 6145 6150

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His Lys Thr Ile Ala Thr Gln Thr Gly Pro Ser Gly Val Thr Ser
6155 6160 6165

Leu Gly Gln Leu Thr Leu Asp Thr Ser Thr Ile Ala Thr Ser Ala
6170 6175 6180

Gly Thr Pro Ser Ala Arg Thr Gln Asp Phe Val Asp Ser Glu Thr
6185 6190 6195

Thr Ser Val Met Asn Asn Asp Leu Asn Asp Val Leu Lys Thr Ser
6200 6205 6210

Pro Phe Ser Ala Glu Glu Ala Asn Ser Leu Ser Ser Gln Ala Pro
6215 6220 6225

Leu Leu Val Thr Thr Ser Pro Ser Pro Val Thr Ser Thr Leu Gln
6230 6235 6240

Glu His Ser Thr Ser Ser Leu Val Ser Val Thr Ser Val Pro Thr
6245 6250 6255

Pro Thr Leu Ala Lys Ile Thr Asp Met Asp Thr Asn Leu Glu Pro
6260 6265 6270

Val Thr Arg Ser Pro Gln Asn Leu Arg Asn Thr Leu Ala Thr Ser
6275 6280 6285

Glu Ala Thr Thr Asp Thr His Thr Met His Pro Ser Ile Asn Thr
6290 6295 6300

Ala Met Ala Asn Val Gly Thr Thr Ser Ser Pro Asn Glu Phe Tyr
6305 6310 6315

Phe Thr Val Ser Pro Asp Ser Asp Pro Tyr Lys Ala Thr Ser Ala
6320 6325 6330

Val Val Ile Thr Ser Thr Ser Gly Asp Ser Ile Val Ser Thr Ser
6335 6340 6345

Met Pro Arg Ser Ser Ala Met Lys Lys Ile Glu Ser Glu Thr Thr
6350 6355 6360

Phe Ser Leu Ile Phe Arg Leu Arg Glu Thr Ser Thr Ser Gln Lys
6365 6370 6375

Ile Gly Ser Ser Ser Asp Thr Ser Thr Val Phe Asp Lys Ala Phe
6380 6385 6390

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Thr Ala Ala Thr Thr Glu Val Ser Arg Thr Glu Leu Thr Ser Ser
6395 6400 6405

Ser Arg Thr Ser Ile Gln Gly Thr Glu Lys Pro Thr Met Ser Pro
6410 6415 6420

Asp Thr Ser Thr Arg Ser Val Thr Met Leu Ser Thr Phe Ala Gly
6425 6430 6435

Leu Thr Lys Ser Glu Glu Arg Thr Ile Ala Thr Gln Thr Gly Pro
6440 6445 6450

His Arg Ala Thr Ser Gln Gly Thr Leu Thr Trp Asp Thr Ser Ile
6455 6460 6465

Thr Thr Ser Gln Ala Gly Thr His Ser Ala Met Thr His Gly Phe
6470 6475 6480

Ser Gln Leu Asp Leu Ser Thr Leu Thr Ser Arg Val Pro Glu Tyr
6485 6490 6495

Ile Ser Gly Thr Ser Pro Pro Ser Val Glu Lys Thr Ser Ser Ser
6500 6505 6510

Ser Ser Leu Leu Ser Leu Pro Ala Ile Thr Ser Pro Ser Pro Val
6515 6520 6525

Pro Thr Thr Leu Pro Glu Ser Arg Pro Ser Ser Pro Val His Leu
6530 6535 6540

Thr Ser Leu Pro Thr Ser Gly Leu Val Lys Thr Thr Asp Met Leu
6545 6550 6555

Ala Ser Val Ala Ser Leu Pro Pro Asn Leu Gly Ser Thr Ser His
6560 6565 6570

Lys Ile Pro Thr Thr Ser Glu Asp Ile Lys Asp Thr Glu Lys Met
6575 6580 6585

Tyr Pro Ser Thr Asn Ile Ala Val Thr Asn Val Gly Thr Thr Thr
6590 6595 6600

Ser Glu Lys Glu Ser Tyr Ser Ser Val Pro Ala Tyr Ser Glu Pro
6605 6610 6615

Pro Lys Val Thr Ser Pro Met Val Thr Ser Phe Asn Ile Arg Asp
6620 6625 6630

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Thr Ile Val Ser Thr Ser Met Pro Gly Ser Ser Glu Ile Thr Arg
 6635 6640 6645
 Ile Glu Met Glu Ser Thr Phe Ser Leu Ala His Gly Leu Lys Gly
 6650 6655 6660
 Thr Ser Thr Ser Gln Asp Pro Ile Val Ser Thr Glu Lys Ser Ala
 6665 6670 6675
 Val Leu His Lys Leu Thr Thr Gly Ala Thr Glu Thr Ser Arg Thr
 6680 6685 6690
 Glu Val Ala Ser Ser Arg Arg Thr Ser Ile Pro Gly Pro Asp His
 6695 6700 6705
 Ser Thr Glu Ser Pro Asp Ile Ser Thr Glu Val Ile Pro Ser Leu
 6710 6715 6720
 Pro Ile Ser Leu Gly Ile Thr Glu Ser Ser Asn Met Thr Ile Ile
 6725 6730 6735
 Thr Arg Thr Gly Pro Pro Leu Gly Ser Thr Ser Gln Gly Thr Phe
 6740 6745 6750
 Thr Leu Asp Thr Pro Thr Thr Ser Ser Arg Ala Gly Thr His Ser
 6755 6760 6765
 Met Ala Thr Gln Glu Phe Pro His Ser Glu Met Thr Thr Val Met
 6770 6775 6780
 Asn Lys Asp Pro Glu Ile Leu Ser Trp Thr Ile Pro Pro Ser Ile
 6785 6790 6795
 Glu Lys Thr Ser Phe Ser Ser Ser Leu Met Pro Ser Pro Ala Met
 6800 6805 6810
 Thr Ser Pro Pro Val Ser Ser Thr Leu Pro Lys Thr Ile His Thr
 6815 6820 6825
 Thr Pro Ser Pro Met Thr Ser Leu Leu Thr Pro Ser Leu Val Met
 6830 6835 6840
 Thr Thr Asp Thr Leu Gly Thr Ser Pro Glu Pro Thr Thr Ser Ser
 6845 6850 6855
 Pro Pro Asn Leu Ser Ser Thr Ser His Val Ile Leu Thr Thr Asp
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6860 6865 6870
 Glu Asp Thr Thr Ala Ile Glu Ala Met His Pro Ser Thr Ser Thr
 6875 6880 6885
 Ala Ala Thr Asn Val Glu Thr Thr Cys Ser Gly His Gly Ser Gln
 6890 6895 6900
 Ser Ser Val Leu Thr Asp Ser Glu Lys Thr Lys Ala Thr Ala Pro
 6905 6910 6915
 Met Asp Thr Thr Ser Thr Met Gly His Thr Thr Val Ser Thr Ser
 6920 6925 6930
 Met Ser Val Ser Ser Glu Thr Thr Lys Ile Lys Arg Glu Ser Thr
 6935 6940 6945
 Tyr Ser Leu Thr Pro Gly Leu Arg Glu Thr Ser Ile Ser Gln Asn
 6950 6955 6960
 Ala Ser Phe Ser Thr Asp Thr Ser Ile Val Leu Ser Glu Val Pro
 6965 6970 6975
 Thr Gly Thr Thr Ala Glu Val Ser Arg Thr Glu Val Thr Ser Ser
 6980 6985 6990
 Gly Arg Thr Ser Ile Pro Gly Pro Ser Gln Ser Thr Val Leu Pro
 6995 7000 7005
 Glu Ile Ser Thr Arg Thr Met Thr Arg Leu Phe Ala Ser Pro Thr
 7010 7015 7020
 Met Thr Glu Ser Ala Glu Met Thr Ile Pro Thr Gln Thr Gly Pro
 7025 7030 7035
 Ser Gly Ser Thr Ser Gln Asp Thr Leu Thr Leu Asp Thr Ser Thr
 7040 7045 7050
 Thr Lys Ser Gln Ala Lys Thr His Ser Thr Leu Thr Gln Arg Phe
 7055 7060 7065
 Pro His Ser Glu Met Thr Thr Leu Met Ser Arg Gly Pro Gly Asp
 7070 7075 7080
 Met Ser Trp Gln Ser Ser Pro Ser Leu Glu Asn Pro Ser Ser Leu
 7085 7090 7095

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Pro Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Pro Ile
 7100 7105 7110
 Ser Ser Thr Leu Pro Val Thr Ile Ser Ser Ser Pro Leu Pro Val
 7115 7120 7125
 Thr Ser Leu Leu Thr Ser Ser Pro Val Thr Thr Thr Asp Met Leu
 7130 7135 7140
 His Thr Ser Pro Glu Leu Val Thr Ser Ser Pro Pro Lys Leu Ser
 7145 7150 7155
 His Thr Ser Asp Glu Arg Leu Thr Thr Gly Lys Asp Thr Thr Asn
 7160 7165 7170
 Thr Glu Ala Val His Pro Ser Thr Asn Thr Ala Ala Ser Asn Val
 7175 7180 7185
 Glu Ile Pro Ser Phe Gly His Glu Ser Pro Ser Ser Ala Leu Ala
 7190 7195 7200
 Asp Ser Glu Thr Ser Lys Ala Thr Ser Pro Met Phe Ile Thr Ser
 7205 7210 7215
 Thr Gln Glu Asp Thr Thr Val Ala Ile Ser Thr Pro His Phe Leu
 7220 7225 7230
 Glu Thr Ser Arg Ile Gln Lys Glu Ser Ile Ser Ser Leu Ser Pro
 7235 7240 7245
 Lys Leu Arg Glu Thr Gly Ser Ser Val Glu Thr Ser Ser Ala Ile
 7250 7255 7260
 Glu Thr Ser Ala Val Leu Ser Glu Val Ser Ile Gly Ala Thr Thr
 7265 7270 7275
 Glu Ile Ser Arg Thr Glu Val Thr Ser Ser Ser Arg Thr Ser Ile
 7280 7285 7290
 Ser Gly Ser Ala Glu Ser Thr Met Leu Pro Glu Ile Ser Thr Thr
 7295 7300 7305
 Arg Lys Ile Ile Lys Phe Pro Thr Ser Pro Ile Leu Ala Glu Ser
 7310 7315 7320
 Ser Glu Met Thr Ile Lys Thr Gln Thr Ser Pro Pro Gly Ser Thr
 7325 7330 7335

022438.43867(pct2).ST25.txt

Ser Glu Ser Thr Phe Thr Leu Asp Thr Ser Thr Thr Pro Ser Leu
 7340 7345 7350
 Val Ile Thr His Ser Thr Met Thr Gln Arg Leu Pro His Ser Glu
 7355 7360 7365
 Ile Thr Thr Leu Val Ser Arg Gly Ala Gly Asp Val Pro Arg Pro
 7370 7375 7380
 Ser Ser Leu Pro Val Glu Glu Thr Ser Pro Pro Ser Ser Gln Leu
 7385 7390 7395
 Ser Leu Ser Ala Met Ile Ser Pro Ser Pro Val Ser Ser Thr Leu
 7400 7405 7410
 Pro Ala Ser Ser His Ser Ser Ser Ala Ser Val Thr Ser Pro Leu
 7415 7420 7425
 Thr Pro Gly Gln Val Lys Thr Thr Glu Val Leu Asp Ala Ser Ala
 7430 7435 7440
 Glu Pro Glu Thr Ser Ser Pro Pro Ser Leu Ser Ser Thr Ser Val
 7445 7450 7455
 Glu Ile Leu Ala Thr Ser Glu Val Thr Thr Asp Thr Glu Lys Ile
 7460 7465 7470
 His Pro Phe Pro Asn Thr Ala Val Thr Lys Val Gly Thr Ser Ser
 7475 7480 7485
 Ser Gly His Glu Ser Pro Ser Ser Val Leu Pro Asp Ser Glu Thr
 7490 7495 7500
 Thr Lys Ala Thr Ser Ala Met Gly Thr Ile Ser Ile Met Gly Asp
 7505 7510 7515
 Thr Ser Val Ser Thr Leu Thr Pro Ala Leu Ser Asn Thr Arg Lys
 7520 7525 7530
 Ile Gln Ser Glu Pro Ala Ser Ser Leu Thr Thr Arg Leu Arg Glu
 7535 7540 7545
 Thr Ser Thr Ser Glu Glu Thr Ser Leu Ala Thr Glu Ala Asn Thr
 7550 7555 7560
 Val Leu Ser Lys Val Ser Thr Gly Ala Thr Thr Glu Val Ser Arg
 7565 7570 7575

022438.43867(pct2).ST25.txt

Thr Glu Ala Ile Ser Phe Ser Arg Thr Ser Met Ser Gly Pro Glu
 7580 7585 7590
 Gln Ser Thr Met Ser Gln Asp Ile Ser Ile Gly Thr Ile Pro Arg
 7595 7600 7605
 Ile Ser Ala Ser Ser Val Leu Thr Glu Ser Ala Lys Met Thr Ile
 7610 7615 7620
 Thr Thr Gln Thr Gly Pro Ser Glu Ser Thr Leu Glu Ser Thr Leu
 7625 7630 7635
 Asn Leu Asn Thr Ala Thr Thr Pro Ser Trp Val Glu Thr His Ser
 7640 7645 7650
 Ile Val Ile Gln Gly Phe Pro His Pro Glu Met Thr Thr Ser Met
 7655 7660 7665
 Gly Arg Gly Pro Gly Gly Val Ser Trp Pro Ser Pro Pro Phe Val
 7670 7675 7680
 Lys Glu Thr Ser Pro Pro Ser Ser Pro Leu Ser Leu Pro Ala Val
 7685 7690 7695
 Thr Ser Pro His Pro Val Ser Thr Thr Phe Leu Ala His Ile Pro
 7700 7705 7710
 Pro Ser Pro Leu Pro Val Thr Ser Leu Leu Thr Ser Gly Pro Ala
 7715 7720 7725
 Thr Thr Thr Asp Ile Leu Gly Thr Ser Thr Glu Pro Gly Thr Ser
 7730 7735 7740
 Ser Ser Ser Ser Leu Ser Thr Thr Ser His Glu Arg Leu Thr Thr
 7745 7750 7755
 Tyr Lys Asp Thr Ala His Thr Glu Ala Val His Pro Ser Thr Asn
 7760 7765 7770
 Thr Gly Gly Thr Asn Val Ala Thr Thr Ser Ser Gly Tyr Lys Ser
 7775 7780 7785
 Gln Ser Ser Val Leu Ala Asp Ser Ser Pro Met Cys Thr Thr Ser
 7790 7795 7800
 Thr Met Gly Asp Thr Ser Val Leu Thr Ser Thr Pro Ala Phe Leu
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7805 7810 7815
 Glu Thr Arg Arg Ile Gln Thr Glu Leu Ala Ser Ser Leu Thr Pro
 7820 7825 7830
 Gly Leu Arg Glu Ser Ser Gly Ser Glu Gly Thr Ser Ser Gly Thr
 7835 7840 7845
 Lys Met Ser Thr Val Leu Ser Lys Val Pro Thr Gly Ala Thr Thr
 7850 7855 7860
 Glu Ile Ser Lys Glu Asp Val Thr Ser Ile Pro Gly Pro Ala Gln
 7865 7870 7875
 Ser Thr Ile Ser Pro Asp Thr Ser Thr Arg Thr Val Ser Trp Phe
 7880 7885 7890
 Ser Thr Ser Pro Val Met Thr Glu Ser Ala Glu Ile Thr Met Asn
 7895 7900 7905
 Thr His Thr Ser Pro Leu Gly Ala Thr Thr Gln Gly Thr Ser Thr
 7910 7915 7920
 Leu Asp Thr Ser Ser Thr Thr Ser Leu Thr Met Thr His Ser Thr
 7925 7930 7935
 Ile Ser Gln Gly Phe Ser His Ser Gln Met Ser Thr Leu Met Arg
 7940 7945 7950
 Arg Gly Pro Glu Asp Val Ser Trp Met Ser Pro Pro Leu Leu Glu
 7955 7960 7965
 Lys Thr Arg Pro Ser Phe Ser Leu Met Ser Ser Pro Ala Thr Thr
 7970 7975 7980
 Ser Pro Ser Pro Val Ser Ser Thr Leu Pro Glu Ser Ile Ser Ser
 7985 7990 7995
 Ser Pro Leu Pro Val Thr Ser Leu Leu Thr Ser Gly Leu Ala Lys
 8000 8005 8010
 Thr Thr Asp Met Leu His Lys Ser Ser Glu Pro Val Thr Asn Ser
 8015 8020 8025
 Pro Ala Asn Leu Ser Ser Thr Ser Val Glu Ile Leu Ala Thr Ser
 8030 8035 8040

022438.43867(pct2).ST25.txt

Glu Val Thr Thr Asp Thr Glu Lys Thr His Pro Ser Ser Asn Arg
 8045 8050 8055
 Thr Val Thr Asp Val Gly Thr Ser Ser Ser Gly His Glu Ser Thr
 8060 8065 8070
 Ser Phe Val Leu Ala Asp Ser Gln Thr Ser Lys Val Thr Ser Pro
 8075 8080 8085
 Met Val Ile Thr Ser Thr Met Glu Asp Thr Ser Val Ser Thr Ser
 8090 8095 8100
 Thr Pro Gly Phe Phe Glu Thr Ser Arg Ile Gln Thr Glu Pro Thr
 8105 8110 8115
 Ser Ser Leu Thr Leu Gly Leu Arg Lys Thr Ser Ser Ser Glu Gly
 8120 8125 8130
 Thr Ser Leu Ala Thr Glu Met Ser Thr Val Leu Ser Gly Val Pro
 8135 8140 8145
 Thr Gly Ala Thr Ala Glu Val Ser Arg Thr Glu Val Thr Ser Ser
 8150 8155 8160
 Ser Arg Thr Ser Ile Ser Gly Phe Ala Gln Leu Thr Val Ser Pro
 8165 8170 8175
 Glu Thr Ser Thr Glu Thr Ile Thr Arg Leu Pro Thr Ser Ser Ile
 8180 8185 8190
 Met Thr Glu Ser Ala Glu Met Met Ile Lys Thr Gln Thr Asp Pro
 8195 8200 8205
 Pro Gly Ser Thr Pro Glu Ser Thr His Thr Val Asp Ile Ser Thr
 8210 8215 8220
 Thr Pro Asn Trp Val Glu Thr His Ser Thr Val Thr Gln Arg Phe
 8225 8230 8235
 Ser His Ser Glu Met Thr Thr Leu Val Ser Arg Ser Pro Gly Asp
 8240 8245 8250
 Met Leu Trp Pro Ser Gln Ser Ser Val Glu Glu Thr Ser Ser Ala
 8255 8260 8265
 Ser Ser Leu Leu Ser Leu Pro Ala Thr Thr Ser Pro Ser Pro Val
 8270 8275 8280

022438.43867(pct2).ST25.txt

Ser Ser Thr Leu Val Glu Asp Phe Pro Ser Ala Ser Leu Pro Val
 8285 8290 8295
 Thr Ser Leu Leu Thr Pro Gly Leu Val Ile Thr Thr Asp Arg Met
 8300 8305 8310
 Gly Ile Ser Arg Glu Pro Gly Thr Ser Ser Thr Ser Asn Leu Ser
 8315 8320 8325
 Ser Thr Ser His Glu Arg Leu Thr Thr Leu Glu Asp Thr Val Asp
 8330 8335 8340
 Thr Glu Ala Met Gln Pro Ser Thr His Thr Ala Val Thr Asn Val
 8345 8350 8355
 Arg Thr Ser Ile Ser Gly His Glu Ser Gln Ser Ser Val Leu Ser
 8360 8365 8370
 Asp Ser Glu Thr Pro Lys Ala Thr Ser Ser Met Gly Thr Thr Tyr
 8375 8380 8385
 Thr Met Gly Glu Thr Ser Val Ser Ile Ser Thr Ser Asp Phe Phe
 8390 8395 8400
 Glu Thr Ser Arg Val Gln Ile Glu Pro Thr Ser Ser Leu Thr Ser
 8405 8410 8415
 Gly Leu Arg Glu Thr Ser Ser Ser Glu Arg Ile Ser Ser Ala Thr
 8420 8425 8430
 Glu Gly Ser Thr Val Leu Ser Glu Val Pro Ser Gly Ala Thr Thr
 8435 8440 8445
 Glu Val Ser Arg Thr Glu Val Ile Ser Ser Arg Gly Thr Ser Met
 8450 8455 8460
 Ser Gly Pro Asp Gln Phe Thr Ile Ser Pro Asp Ile Ser Thr Glu
 8465 8470 8475
 Ala Ile Thr Arg Leu Ser Thr Ser Pro Ile Met Thr Glu Ser Ala
 8480 8485 8490
 Glu Ser Ala Ile Thr Ile Glu Thr Gly Ser Pro Gly Ala Thr Ser
 8495 8500 8505
 Glu Gly Thr Leu Thr Leu Asp Thr Ser Thr Thr Thr Phe Trp Ser
 8510 8515 8520

022438.43867(pct2).ST25.txt

Gly Thr His Ser Thr Ala Ser Pro Gly Phe Ser His Ser Glu Met
8525 8530 8535

Thr Thr Leu Met Ser Arg Thr Pro Gly Asp Val Pro Trp Pro Ser
8540 8545 8550

Leu Pro Ser Val Glu Glu Ala Ser Ser Val Ser Ser Ser Leu Ser
8555 8560 8565

Ser Pro Ala Met Thr Ser Thr Ser Phe Phe Ser Ala Leu Pro Glu
8570 8575 8580

Ser Ile Ser Ser Ser Pro His Pro Val Thr Ala Leu Leu Thr Leu
8585 8590 8595

Gly Pro Val Lys Thr Thr Asp Met Leu Arg Thr Ser Ser Glu Pro
8600 8605 8610

Glu Thr Ser Ser Pro Pro Asn Leu Ser Ser Thr Ser Ala Glu Ile
8615 8620 8625

Leu Ala Thr Ser Glu Val Thr Lys Asp Arg Glu Lys Ile His Pro
8630 8635 8640

Ser Ser Asn Thr Pro Val Val Asn Val Gly Thr Val Ile Tyr Lys
8645 8650 8655

His Leu Ser Pro Ser Ser Val Leu Ala Asp Leu Val Thr Thr Lys
8660 8665 8670

Pro Thr Ser Pro Met Ala Thr Thr Ser Thr Leu Gly Asn Thr Ser
8675 8680 8685

Val Ser Thr Ser Thr Pro Ala Phe Pro Glu Thr Met Met Thr Gln
8690 8695 8700

Pro Thr Ser Ser Leu Thr Ser Gly Leu Arg Glu Ile Ser Thr Ser
8705 8710 8715

Gln Glu Thr Ser Ser Ala Thr Glu Arg Ser Ala Ser Leu Ser Gly
8720 8725 8730

Met Pro Thr Gly Ala Thr Thr Lys Val Ser Arg Thr Glu Ala Leu
8735 8740 8745

Ser Leu Gly Arg Thr Ser Thr Pro Gly Pro Ala Gln Ser Thr Ile
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8750 022438.43867(pct2).ST25.txt
 8755 8760
 Ser Pro Glu Ile Ser Thr Glu Thr Ile Thr Arg Ile Ser Thr Pro
 8765 8770 8775
 Leu Thr Thr Thr Gly Ser Ala Glu Met Thr Ile Thr Pro Lys Thr
 8780 8785 8790
 Gly His Ser Gly Ala Ser Ser Gln Gly Thr Phe Thr Leu Asp Thr
 8795 8800 8805
 Ser Ser Arg Ala Ser Trp Pro Gly Thr His Ser Ala Ala Thr His
 8810 8815 8820
 Arg Ser Pro His Ser Gly Met Thr Thr Pro Met Ser Arg Gly Pro
 8825 8830 8835
 Glu Asp Val Ser Trp Pro Ser Arg Pro Ser Val Glu Lys Thr Ser
 8840 8845 8850
 Pro Pro Ser Ser Leu Val Ser Leu Ser Ala Val Thr Ser Pro Ser
 8855 8860 8865
 Pro Leu Tyr Ser Thr Pro Ser Glu Ser Ser His Ser Ser Pro Leu
 8870 8875 8880
 Arg Val Thr Ser Leu Phe Thr Pro Val Met Met Lys Thr Thr Asp
 8885 8890 8895
 Met Leu Asp Thr Ser Leu Glu Pro Val Thr Thr Ser Pro Pro Ser
 8900 8905 8910
 Met Asn Ile Thr Ser Asp Glu Ser Leu Ala Thr Ser Lys Ala Thr
 8915 8920 8925
 Met Glu Thr Glu Ala Ile Gln Leu Ser Glu Asn Thr Ala Val Thr
 8930 8935 8940
 Gln Met Gly Thr Ile Ser Ala Arg Gln Glu Phe Tyr Ser Ser Tyr
 8945 8950 8955
 Pro Gly Leu Pro Glu Pro Ser Lys Val Thr Ser Pro Val Val Thr
 8960 8965 8970
 Ser Ser Thr Ile Lys Asp Ile Val Ser Thr Thr Ile Pro Ala Ser
 8975 8980 8985

022438.43867(pct2).ST25.txt

Ser Glu Ile Thr Arg Ile Glu Met Glu Ser Thr Ser Thr Leu Thr
 8990 8995 9000
 Pro Thr Pro Arg Glu Thr Ser Thr Ser Gln Glu Ile His Ser Ala
 9005 9010 9015
 Thr Lys Pro Ser Thr Val Pro Tyr Lys Ala Leu Thr Ser Ala Thr
 9020 9025 9030
 Ile Glu Asp Ser Met Thr Gln Val Met Ser Ser Ser Arg Gly Pro
 9035 9040 9045
 Ser Pro Asp Gln Ser Thr Met Ser Gln Asp Ile Ser Thr Glu Val
 9050 9055 9060
 Ile Thr Arg Leu Ser Thr Ser Pro Ile Lys Ala Glu Ser Thr Glu
 9065 9070 9075
 Met Thr Ile Thr Thr Gln Thr Gly Ser Pro Gly Ala Thr Ser Arg
 9080 9085 9090
 Gly Thr Leu Thr Leu Asp Thr Ser Thr Thr Phe Met Ser Gly Thr
 9095 9100 9105
 His Ser Thr Ala Ser Gln Gly Phe Ser His Ser Gln Met Thr Ala
 9110 9115 9120
 Leu Met Ser Arg Thr Pro Gly Asp Val Pro Trp Leu Ser His Pro
 9125 9130 9135
 Ser Val Glu Glu Ala Ser Ser Ala Ser Phe Ser Leu Ser Ser Pro
 9140 9145 9150
 Val Met Thr Ser Ser Ser Pro Val Ser Ser Thr Leu Pro Asp Ser
 9155 9160 9165
 Ile His Ser Ser Ser Leu Pro Val Thr Ser Leu Leu Thr Ser Gly
 9170 9175 9180
 Leu Val Lys Thr Thr Glu Leu Leu Gly Thr Ser Ser Glu Pro Glu
 9185 9190 9195
 Thr Ser Ser Pro Pro Asn Leu Ser Ser Thr Ser Ala Glu Ile Leu
 9200 9205 9210
 Ala Thr Thr Glu Val Thr Thr Asp Thr Glu Lys Leu Glu Met Thr
 9215 9220 9225

022438.43867(pct2).ST25.txt

Asn Val Val Thr Ser Gly Tyr Thr His Glu Ser Pro Ser Ser Val
9230 9235 9240

Leu Ala Asp Ser Val Thr Thr Lys Ala Thr Ser Ser Met Gly Ile
9245 9250 9255

Thr Tyr Pro Thr Gly Asp Thr Asn Val Leu Thr Ser Thr Pro Ala
9260 9265 9270

Phe Ser Asp Thr Ser Arg Ile Gln Thr Lys Ser Lys Leu Ser Leu
9275 9280 9285

Thr Pro Gly Leu Met Glu Thr Ser Ile Ser Glu Glu Thr Ser Ser
9290 9295 9300

Ala Thr Glu Lys Ser Thr Val Leu Ser Ser Val Pro Thr Gly Ala
9305 9310 9315

Thr Thr Glu Val Ser Arg Thr Glu Ala Ile Ser Ser Ser Arg Thr
9320 9325 9330

Ser Ile Pro Gly Pro Ala Gln Ser Thr Met Ser Ser Asp Thr Ser
9335 9340 9345

Met Glu Thr Ile Thr Arg Ile Ser Thr Pro Leu Thr Arg Lys Glu
9350 9355 9360

Ser Thr Asp Met Ala Ile Thr Pro Lys Thr Gly Pro Ser Gly Ala
9365 9370 9375

Thr Ser Gln Gly Thr Phe Thr Leu Asp Ser Ser Ser Thr Ala Ser
9380 9385 9390

Trp Pro Gly Thr His Ser Ala Thr Thr Gln Arg Phe Pro Gln Ser
9395 9400 9405

Val Val Thr Thr Pro Met Ser Arg Gly Pro Glu Asp Val Ser Trp
9410 9415 9420

Pro Ser Pro Leu Ser Val Glu Lys Asn Ser Pro Pro Ser Ser Leu
9425 9430 9435

Val Ser Ser Ser Ser Val Thr Ser Pro Ser Pro Leu Tyr Ser Thr
9440 9445 9450

Pro Ser Gly Ser Ser His Ser Ser Pro Val Pro Val Thr Ser Leu
9455 9460 9465

022438.43867(pct2).ST25.txt

Phe Thr Ser Ile Met Met Lys Ala Thr Asp Met Leu Asp Ala Ser
 9470 9475 9480
 Leu Glu Pro Glu Thr Thr Ser Ala Pro Asn Met Asn Ile Thr Ser
 9485 9490 9495
 Asp Glu Ser Leu Ala Thr Ser Lys Ala Thr Thr Glu Thr Glu Ala
 9500 9505 9510
 Ile His Val Phe Glu Asn Thr Ala Ala Ser His Val Glu Thr Thr
 9515 9520 9525
 Ser Ala Thr Glu Glu Leu Tyr Ser Ser Ser Pro Gly Phe Ser Glu
 9530 9535 9540
 Pro Thr Lys Val Ile Ser Pro Val Val Thr Ser Ser Ser Ile Arg
 9545 9550 9555
 Asp Asn Met Val Ser Thr Thr Met Pro Gly Ser Ser Gly Ile Thr
 9560 9565 9570
 Arg Ile Glu Ile Glu Ser Met Ser Ser Leu Thr Pro Gly Leu Arg
 9575 9580 9585
 Glu Thr Arg Thr Ser Gln Asp Ile Thr Ser Ser Thr Glu Thr Ser
 9590 9595 9600
 Thr Val Leu Tyr Lys Met Ser Ser Gly Ala Thr Pro Glu Val Ser
 9605 9610 9615
 Arg Thr Glu Val Met Pro Ser Ser Arg Thr Ser Ile Pro Gly Pro
 9620 9625 9630
 Ala Gln Ser Thr Met Ser Leu Asp Ile Ser Asp Glu Val Val Thr
 9635 9640 9645
 Arg Leu Ser Thr Ser Pro Ile Met Thr Glu Ser Ala Glu Ile Thr
 9650 9655 9660
 Ile Thr Thr Gln Thr Gly Tyr Ser Leu Ala Thr Ser Gln Val Thr
 9665 9670 9675
 Leu Pro Leu Gly Thr Ser Met Thr Phe Leu Ser Gly Thr His Ser
 9680 9685 9690
 Thr Met Ser Gln Gly Leu Ser His Ser Glu Met Thr Asn Leu Met
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9695 022438.43867(pct2).ST25.txt
 9700 9705
 Ser Arg Gly Pro Glu Ser Leu Ser Trp Thr Ser Pro Arg Phe Val
 9710 9715 9720
 Glu Thr Thr Arg Ser Ser Ser Ser Leu Thr Ser Leu Pro Leu Thr
 9725 9730 9735
 Thr Ser Leu Ser Pro Val Ser Ser Thr Leu Leu Asp Ser Ser Pro
 9740 9745 9750
 Ser Ser Pro Leu Pro Val Thr Ser Leu Ile Leu Pro Gly Leu Val
 9755 9760 9765
 Lys Thr Thr Glu Val Leu Asp Thr Ser Ser Glu Pro Lys Thr Ser
 9770 9775 9780
 Ser Ser Pro Asn Leu Ser Ser Thr Ser Val Glu Ile Pro Ala Thr
 9785 9790 9795
 Ser Glu Ile Met Thr Asp Thr Glu Lys Ile His Pro Ser Ser Asn
 9800 9805 9810
 Thr Ala Val Ala Lys Val Arg Thr Ser Ser Ser Val His Glu Ser
 9815 9820 9825
 His Ser Ser Val Leu Ala Asp Ser Glu Thr Thr Ile Thr Ile Pro
 9830 9835 9840
 Ser Met Gly Ile Thr Ser Ala Val Asp Asp Thr Thr Val Phe Thr
 9845 9850 9855
 Ser Asn Pro Ala Phe Ser Glu Thr Arg Arg Ile Pro Thr Glu Pro
 9860 9865 9870
 Thr Phe Ser Leu Thr Pro Gly Phe Arg Glu Thr Ser Thr Ser Glu
 9875 9880 9885
 Glu Thr Thr Ser Ile Thr Glu Thr Ser Ala Val Leu Tyr Gly Val
 9890 9895 9900
 Pro Thr Ser Ala Thr Thr Glu Val Ser Met Thr Glu Ile Met Ser
 9905 9910 9915
 Ser Asn Arg Thr His Ile Pro Asp Ser Asp Gln Ser Thr Met Ser
 9920 9925 9930

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Pro Asp Ile Ile Thr Glu Val Ile Thr Arg Leu Ser Ser Ser
 9935 9940 9945

Met Met Ser Glu Ser Thr Gln Met Thr Ile Thr Thr Gln Lys Ser
 9950 9955 9960

Ser Pro Gly Ala Thr Ala Gln Ser Thr Leu Thr Leu Ala Thr Thr
 9965 9970 9975

Thr Ala Pro Leu Ala Arg Thr His Ser Thr Val Pro Pro Arg Phe
 9980 9985 9990

Leu His Ser Glu Met Thr Thr Leu Met Ser Arg Ser Pro Glu Asn
 9995 10000 10005

Pro Ser Trp Lys Ser Ser Pro Phe Val Glu Lys Thr Ser Ser Ser
 10010 10015 10020

Ser Ser Leu Leu Ser Leu Pro Val Thr Thr Ser Pro Ser Val Ser
 10025 10030 10035

Ser Thr Leu Pro Gln Ser Ile Pro Ser Ser Ser Phe Ser Val Thr
 10040 10045 10050

Ser Leu Leu Thr Pro Gly Met Val Lys Thr Thr Asp Thr Ser Thr
 10055 10060 10065

Glu Pro Gly Thr Ser Leu Ser Pro Asn Leu Ser Gly Thr Ser Val
 10070 10075 10080

Glu Ile Leu Ala Ala Ser Glu Val Thr Thr Asp Thr Glu Lys Ile
 10085 10090 10095

His Pro Ser Ser Ser Met Ala Val Thr Asn Val Gly Thr Thr Ser
 10100 10105 10110

Ser Gly His Glu Leu Tyr Ser Ser Val Ser Ile His Ser Glu Pro
 10115 10120 10125

Ser Lys Ala Thr Tyr Pro Val Gly Thr Pro Ser Ser Met Ala Glu
 10130 10135 10140

Thr Ser Ile Ser Thr Ser Met Pro Ala Asn Phe Glu Thr Thr Gly
 10145 10150 10155

Phe Glu Ala Glu Pro Phe Ser His Leu Thr Ser Gly Phe Arg Lys
 10160 10165 10170

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Thr Asn Met Ser Leu Asp Thr Ser Ser Val Thr Pro Thr Asn Thr
 10175 10180 10185
 Pro Ser Ser Pro Gly Ser Thr His Leu Leu Gln Ser Ser Lys Thr
 10190 10195 10200
 Asp Phe Thr Ser Ser Ala Lys Thr Ser Ser Pro Asp Trp Pro Pro
 10205 10210 10215
 Ala Ser Gln Tyr Thr Glu Ile Pro Val Asp Ile Ile Thr Pro Phe
 10220 10225 10230
 Asn Ala Ser Pro Ser Ile Thr Glu Ser Thr Gly Ile Thr Ser Phe
 10235 10240 10245
 Pro Glu Ser Arg Phe Thr Met Ser Val Thr Glu Ser Thr His His
 10250 10255 10260
 Leu Ser Thr Asp Leu Leu Pro Ser Ala Glu Thr Ile Ser Thr Gly
 10265 10270 10275
 Thr Val Met Pro Ser Leu Ser Glu Ala Met Thr Ser Phe Ala Thr
 10280 10285 10290
 Thr Gly Val Pro Arg Ala Ile Ser Gly Ser Gly Ser Pro Phe Ser
 10295 10300 10305
 Arg Thr Glu Ser Gly Pro Gly Asp Ala Thr Leu Ser Thr Ile Ala
 10310 10315 10320
 Glu Ser Leu Pro Ser Ser Thr Pro Val Pro Phe Ser Ser Ser Thr
 10325 10330 10335
 Phe Thr Thr Thr Asp Ser Ser Thr Ile Pro Ala Leu His Glu Ile
 10340 10345 10350
 Thr Ser Ser Ser Ala Thr Pro Tyr Arg Val Asp Thr Ser Leu Gly
 10355 10360 10365
 Thr Glu Ser Ser Thr Thr Glu Gly Arg Leu Val Met Val Ser Thr
 10370 10375 10380
 Leu Asp Thr Ser Ser Gln Pro Gly Arg Thr Ser Ser Thr Pro Ile
 10385 10390 10395
 Leu Asp Thr Arg Met Thr Glu Ser Val Glu Leu Gly Thr Val Thr
 10400 10405 10410

022438.43867(pct2).ST25.txt

Ser Ala Tyr Gln Val Pro Ser Leu Ser Thr Arg Leu Thr Arg Thr
 10415 10420 10425
 Asp Gly Ile Met Glu His Ile Thr Lys Ile Pro Asn Glu Ala Ala
 10430 10435 10440
 His Arg Gly Thr Ile Arg Pro Val Lys Gly Pro Gln Thr Ser Thr
 10445 10450 10455
 Ser Pro Ala Ser Pro Lys Gly Leu His Thr Gly Gly Thr Lys Arg
 10460 10465 10470
 Met Glu Thr Thr Thr Thr Ala Leu Lys Thr Thr Thr Thr Ala Leu
 10475 10480 10485
 Lys Thr Thr Ser Arg Ala Thr Leu Thr Thr Ser Val Tyr Thr Pro
 10490 10495 10500
 Thr Leu Gly Thr Leu Thr Pro Leu Asn Ala Ser Arg Gln Met Ala
 10505 10510 10515
 Ser Thr Ile Leu Thr Glu Met Met Ile Thr Thr Pro Tyr Val Phe
 10520 10525 10530
 Pro Asp Val Pro Glu Thr Thr Ser Ser Leu Ala Thr Ser Leu Gly
 10535 10540 10545
 Ala Glu Thr Ser Thr Ala Leu Pro Arg Thr Thr Pro Ser Val Leu
 10550 10555 10560
 Asn Arg Glu Ser Glu Thr Thr Ala Ser Leu Val Ser Arg Ser Gly
 10565 10570 10575
 Ala Glu Arg Ser Pro Val Ile Gln Thr Leu Asp Val Ser Ser Ser
 10580 10585 10590
 Glu Pro Asp Thr Thr Ala Ser Trp Val Ile His Pro Ala Glu Thr
 10595 10600 10605
 Ile Pro Thr Val Ser Lys Thr Thr Pro Asn Phe Phe His Ser Glu
 10610 10615 10620
 Leu Asp Thr Val Ser Ser Thr Ala Thr Ser His Gly Ala Asp Val
 10625 10630 10635
 Ser Ser Ala Ile Pro Thr Asn Ile Ser Pro Ser Glu Leu Asp Ala
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10640		10645		10650	
Leu Thr 10655	Pro Leu Val Thr	Ile 10660	Ser Gly Thr Asp	Thr 10665	Ser Thr Thr
Phe Pro 10670	Thr Leu Thr Lys	Ser 10675	Pro His Glu Thr	Glu 10680	Thr Arg Thr
Thr Trp 10685	Leu Thr His Pro	Ala 10690	Glu Thr Ser Ser	Thr 10695	Ile Pro Arg
Thr Ile 10700	Pro Asn Phe Ser	His 10705	His Glu Ser Asp	Ala 10710	Thr Pro Ser
Ile Ala 10715	Thr Ser Pro Gly	Ala 10720	Glu Thr Ser Ser	Ala 10725	Ile Pro Ile
Met Thr 10730	Val Ser Pro Gly	Ala 10735	Glu Asp Leu Val	Thr 10740	Ser Gln Val
Thr Ser 10745	Ser Gly Thr Asp	Arg 10750	Asn Met Thr Ile	Pro 10755	Thr Leu Thr
Leu Ser 10760	Pro Gly Glu Pro	Lys 10765	Thr Ile Ala Ser	Leu 10770	Val Thr His
Pro Glu 10775	Ala Gln Thr Ser	Ser 10780	Ala Ile Pro Thr	Ser 10785	Thr Ile Ser
Pro Ala 10790	Val Ser Arg Leu	Val 10795	Thr Ser Met Val	Thr 10800	Ser Leu Ala
Ala Lys 10805	Thr Ser Thr Thr	Asn 10810	Arg Ala Leu Thr	Asn 10815	Ser Pro Gly
Glu Pro 10820	Ala Thr Thr Val	Ser 10825	Leu Val Thr His	Pro 10830	Ala Gln Thr
Ser Pro 10835	Thr Val Pro Trp	Thr 10840	Thr Ser Ile Phe	Phe 10845	His Ser Lys
Ser Asp 10850	Thr Thr Pro Ser	Met 10855	Thr Thr Ser His	Gly 10860	Ala Glu Ser
Ser Ser 10865	Ala Val Pro Thr	Pro 10870	Thr Val Ser Thr	Glu 10875	Val Pro Gly

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Val	Val	Thr	Pro	Leu	Val	Thr	Ser	Ser	Arg	Ala	Val	Ile	Ser	Thr
10880						10885					10890			
Thr	Ile	Pro	Ile	Leu	Thr	Leu	Ser	Pro	Gly	Glu	Pro	Glu	Thr	Thr
10895						10900					10905			
Pro	Ser	Met	Ala	Thr	Ser	His	Gly	Glu	Glu	Ala	Ser	Ser	Ala	Ile
10910						10915					10920			
Pro	Thr	Pro	Thr	Val	Ser	Pro	Gly	Val	Pro	Gly	Val	Val	Thr	Ser
10925						10930					10935			
Leu	Val	Thr	Ser	Ser	Arg	Ala	Val	Thr	Ser	Thr	Thr	Ile	Pro	Ile
10940						10945					10950			
Leu	Thr	Phe	Ser	Leu	Gly	Glu	Pro	Glu	Thr	Thr	Pro	Ser	Met	Ala
10955						10960					10965			
Thr	Ser	His	Gly	Thr	Glu	Ala	Gly	Ser	Ala	Val	Pro	Thr	Val	Leu
10970						10975					10980			
Pro	Glu	Val	Pro	Gly	Met	Val	Thr	Ser	Leu	Val	Ala	Ser	Ser	Arg
10985						10990					10995			
Ala	Val	Thr	Ser	Thr	Thr	Leu	Pro	Thr	Leu	Thr	Leu	Ser	Pro	Gly
11000						11005					11010			
Glu	Pro	Glu	Thr	Thr	Pro	Ser	Met	Ala	Thr	Ser	His	Gly	Ala	Glu
11015						11020					11025			
Ala	Ser	Ser	Thr	Val	Pro	Thr	Val	Ser	Pro	Glu	Val	Pro	Gly	Val
11030						11035					11040			
Val	Thr	Ser	Leu	Val	Thr	Ser	Ser	Ser	Gly	Val	Asn	Ser	Thr	Ser
11045						11050					11055			
Ile	Pro	Thr	Leu	Ile	Leu	Ser	Pro	Gly	Glu	Leu	Glu	Thr	Thr	Pro
11060						11065					11070			
Ser	Met	Ala	Thr	Ser	His	Gly	Ala	Glu	Ala	Ser	Ser	Ala	Val	Pro
11075						11080					11085			
Thr	Pro	Thr	Val	Ser	Pro	Gly	Val	Ser	Gly	Val	Val	Thr	Pro	Leu
11090						11095					11100			
Val	Thr	Ser	Ser	Arg	Ala	Val	Thr	Ser	Thr	Thr	Ile	Pro	Ile	Leu
11105						11110					11115			

022438.43867(pct2).ST25.txt

Thr Leu Ser Ser Ser Glu Pro Glu Thr Thr Pro Ser Met Ala Thr
 11120 11125 11130
 Ser His Gly Val Glu Ala Ser Ser Ala Val Leu Thr Val Ser Pro
 11135 11140 11145
 Glu Val Pro Gly Met Val Thr Ser Leu Val Thr Ser Ser Arg Ala
 11150 11155 11160
 Val Thr Ser Thr Thr Ile Pro Thr Leu Thr Ile Ser Ser Asp Glu
 11165 11170 11175
 Pro Glu Thr Thr Thr Ser Leu Val Thr His Ser Glu Ala Lys Met
 11180 11185 11190
 Ile Ser Ala Ile Pro Thr Leu Ala Val Ser Pro Thr Val Gln Gly
 11195 11200 11205
 Leu Val Thr Ser Leu Val Thr Ser Ser Gly Ser Glu Thr Ser Ala
 11210 11215 11220
 Phe Ser Asn Leu Thr Val Ala Ser Ser Gln Pro Glu Thr Ile Asp
 11225 11230 11235
 Ser Trp Val Ala His Pro Gly Thr Glu Ala Ser Ser Val Val Pro
 11240 11245 11250
 Thr Leu Thr Val Ser Thr Gly Glu Pro Phe Thr Asn Ile Ser Leu
 11255 11260 11265
 Val Thr His Pro Ala Glu Ser Ser Ser Thr Leu Pro Arg Thr Thr
 11270 11275 11280
 Ser Arg Phe Ser His Ser Glu Leu Asp Thr Met Pro Ser Thr Val
 11285 11290 11295
 Thr Ser Pro Glu Ala Glu Ser Ser Ser Ala Ile Ser Thr Thr Ile
 11300 11305 11310
 Ser Pro Gly Ile Pro Gly Val Leu Thr Ser Leu Val Thr Ser Ser
 11315 11320 11325
 Gly Arg Asp Ile Ser Ala Thr Phe Pro Thr Val Pro Glu Ser Pro
 11330 11335 11340
 His Glu Ser Glu Ala Thr Ala Ser Trp Val Thr His Pro Ala Val
 11345 11350 11355

022438.43867(pct2).ST25.txt

Thr Ser Thr Thr Val Pro Arg Thr Thr Pro Asn Tyr Ser His Ser
 11360 11365 11370
 Glu Pro Asp Thr Thr Pro Ser Ile Ala Thr Ser Pro Gly Ala Glu
 11375 11380 11385
 Ala Thr Ser Asp Phe Pro Thr Ile Thr Val Ser Pro Asp Val Pro
 11390 11395 11400
 Asp Met Val Thr Ser Gln Val Thr Ser Ser Gly Thr Asp Thr Ser
 11405 11410 11415
 Ile Thr Ile Pro Thr Leu Thr Leu Ser Ser Gly Glu Pro Glu Thr
 11420 11425 11430
 Thr Thr Ser Phe Ile Thr Tyr Ser Glu Thr His Thr Ser Ser Ala
 11435 11440 11445
 Ile Pro Thr Leu Pro Val Ser Pro Gly Ala Ser Lys Met Leu Thr
 11450 11455 11460
 Ser Leu Val Ile Ser Ser Gly Thr Asp Ser Thr Thr Thr Phe Pro
 11465 11470 11475
 Thr Leu Thr Glu Thr Pro Tyr Glu Pro Glu Thr Thr Ala Ile Gln
 11480 11485 11490
 Leu Ile His Pro Ala Glu Thr Asn Thr Met Val Pro Arg Thr Thr
 11495 11500 11505
 Pro Lys Phe Ser His Ser Lys Ser Asp Thr Thr Leu Pro Val Ala
 11510 11515 11520
 Ile Thr Ser Pro Gly Pro Glu Ala Ser Ser Ala Val Ser Thr Thr
 11525 11530 11535
 Thr Ile Ser Pro Asp Met Ser Asp Leu Val Thr Ser Leu Val Pro
 11540 11545 11550
 Ser Ser Gly Thr Asp Thr Ser Thr Thr Phe Pro Thr Leu Ser Glu
 11555 11560 11565
 Thr Pro Tyr Glu Pro Glu Thr Thr Ala Thr Trp Leu Thr His Pro
 11570 11575 11580
 Ala Glu Thr Ser Thr Thr Val Ser Gly Thr Ile Pro Asn Phe Ser
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11585 022438.43867(pct2).ST25.txt
 11590 11595
 His Arg Gly Ser Asp Thr Ala Pro Ser Met Val Thr Ser Pro Gly
 11600 11605 11610
 Val Asp Thr Arg Ser Gly Val Pro Thr Thr Thr Ile Pro Pro Ser
 11615 11620 11625
 Ile Pro Gly Val Val Thr Ser Gln Val Thr Ser Ser Ala Thr Asp
 11630 11635 11640
 Thr Ser Thr Ala Ile Pro Thr Leu Thr Pro Ser Pro Gly Glu Pro
 11645 11650 11655
 Glu Thr Thr Ala Ser Ser Ala Thr His Pro Gly Thr Gln Thr Gly
 11660 11665 11670
 Phe Thr Val Pro Ile Arg Thr Val Pro Ser Ser Glu Pro Asp Thr
 11675 11680 11685
 Met Ala Ser Trp Val Thr His Pro Pro Gln Thr Ser Thr Pro Val
 11690 11695 11700
 Ser Arg Thr Thr Ser Ser Phe Ser His Ser Ser Pro Asp Ala Thr
 11705 11710 11715
 Pro Val Met Ala Thr Ser Pro Arg Thr Glu Ala Ser Ser Ala Val
 11720 11725 11730
 Leu Thr Thr Ile Ser Pro Gly Ala Pro Glu Met Val Thr Ser Gln
 11735 11740 11745
 Ile Thr Ser Ser Gly Ala Ala Thr Ser Thr Thr Val Pro Thr Leu
 11750 11755 11760
 Thr His Ser Pro Gly Met Pro Glu Thr Thr Ala Leu Leu Ser Thr
 11765 11770 11775
 His Pro Arg Thr Glu Thr Ser Lys Thr Phe Pro Ala Ser Thr Val
 11780 11785 11790
 Phe Pro Gln Val Ser Glu Thr Thr Ala Ser Leu Thr Ile Arg Pro
 11795 11800 11805
 Gly Ala Glu Thr Ser Thr Ala Leu Pro Thr Gln Thr Thr Ser Ser
 11810 11815 11820

022438.43867(pct2).ST25.txt

Leu	Phe	Thr	Leu	Leu	Val	Thr	Gly	Thr	Ser	Arg	Val	Asp	Leu	Ser
	11825					11830					11835			
Pro	Thr	Ala	Ser	Pro	Gly	Val	Ser	Ala	Lys	Thr	Ala	Pro	Leu	Ser
	11840					11845					11850			
Thr	His	Pro	Gly	Thr	Glu	Thr	Ser	Thr	Met	Ile	Pro	Thr	Ser	Thr
	11855					11860					11865			
Leu	Ser	Leu	Gly	Leu	Leu	Glu	Thr	Thr	Gly	Leu	Leu	Ala	Thr	Ser
	11870					11875					11880			
Ser	Ser	Ala	Glu	Thr	Ser	Thr	Ser	Thr	Leu	Thr	Leu	Thr	Val	Ser
	11885					11890					11895			
Pro	Ala	Val	Ser	Gly	Leu	Ser	Ser	Ala	Ser	Ile	Thr	Thr	Asp	Lys
	11900					11905					11910			
Pro	Gln	Thr	Val	Thr	Ser	Trp	Asn	Thr	Glu	Thr	Ser	Pro	Ser	Val
	11915					11920					11925			
Thr	Ser	Val	Gly	Pro	Pro	Glu	Phe	Ser	Arg	Thr	Val	Thr	Gly	Thr
	11930					11935					11940			
Thr	Met	Thr	Leu	Ile	Pro	Ser	Glu	Met	Pro	Thr	Pro	Pro	Lys	Thr
	11945					11950					11955			
Ser	His	Gly	Glu	Gly	Val	Ser	Pro	Thr	Thr	Ile	Leu	Arg	Thr	Thr
	11960					11965					11970			
Met	Val	Glu	Ala	Thr	Asn	Leu	Ala	Thr	Thr	Gly	Ser	Ser	Pro	Thr
	11975					11980					11985			
Val	Ala	Lys	Thr	Thr	Thr	Thr	Phe	Asn	Thr	Leu	Ala	Gly	Ser	Leu
	11990					11995					12000			
Phe	Thr	Pro	Leu	Thr	Thr	Pro	Gly	Met	Ser	Thr	Leu	Ala	Ser	Glu
	12005					12010					12015			
Ser	Val	Thr	Ser	Arg	Thr	Ser	Tyr	Asn	His	Arg	Ser	Trp	Ile	Ser
	12020					12025					12030			
Thr	Thr	Ser	Ser	Tyr	Asn	Arg	Arg	Tyr	Trp	Thr	Pro	Ala	Thr	Ser
	12035					12040					12045			
Thr	Pro	Val	Thr	Ser	Thr	Phe	Ser	Pro	Gly	Ile	Ser	Thr	Ser	Ser
	12050					12055					12060			

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Ile Pro Ser Ser Thr Ala Ala Thr Val Pro Phe Met Val Pro Phe
 12065 12070 12075
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
 12080 12085 12090
 Arg His Pro Gly Ser Arg Lys Phe Asn Ala Thr Glu Arg Glu Leu
 12095 12100 12105
 Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr
 12110 12115 12120
 Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp
 12125 12130 12135
 Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp
 12140 12145 12150
 Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 12155 12160 12165
 Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu
 12170 12175 12180
 Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser
 12185 12190 12195
 Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Val Gly
 12200 12205 12210
 Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro Thr Ala Ala Gly
 12215 12220 12225
 Pro Leu Leu Met Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 12230 12235 12240
 Gln Tyr Glu Glu Asp Met Arg Arg Thr Gly Ser Arg Lys Phe Asn
 12245 12250 12255
 Thr Met Glu Ser Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys
 12260 12265 12270
 Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 12275 12280 12285
 Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile
 12290 12295 12300

022438.43867(pct2).ST25.txt

Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu
 12305 12310 12315
 Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu
 12320 12325 12330
 Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly
 12335 12340 12345
 Phe Thr His Gln Ser Ser Val Ser Thr Thr Ser Thr Pro Gly Thr
 12350 12355 12360
 Ser Thr Val Asp Leu Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser
 12365 12370 12375
 Ser Pro Thr Ile Met Ala Ala Gly Pro Leu Leu Val Pro Phe Thr
 12380 12385 12390
 Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly
 12395 12400 12405
 His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
 12410 12415 12420
 Gly Leu Leu Gly Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu
 12425 12430 12435
 Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly
 12440 12445 12450
 Ala Ala Thr Gly Val Asp Ala Ile Cys Ile His His Leu Asp Pro
 12455 12460 12465
 Lys Ser Pro Gly Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser
 12470 12475 12480
 Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp
 12485 12490 12495
 Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val
 12500 12505 12510
 Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr
 12515 12520 12525
 Ser Gly Thr Pro Phe Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro

12530 022438.43867(pct2).ST25.txt
 12535 12540

Leu Leu Val Leu Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys
 12545 12550 12555

Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr
 12560 12565 12570

Thr Glu Arg Val Leu Gln Thr Leu Leu Gly Pro Met Phe Lys Asn
 12575 12580 12585

Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu
 12590 12595 12600

Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys
 12605 12610 12615

Thr His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln
 12620 12625 12630

Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu
 12635 12640 12645

Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe
 12650 12655 12660

Thr His Trp Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser
 12665 12670 12675

Thr Val Asp Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro
 12680 12685 12690

Thr Ala Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 12695 12700 12705

Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser
 12710 12715 12720

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
 12725 12730 12735

Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys
 12740 12745 12750

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
 12755 12760 12765

022438.43867(pct2).ST25.txt

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly
12770 12775 12780

Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn
12785 12790 12795

Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
12800 12805 12810

Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser
12815 12820 12825

Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
12830 12835 12840

Ser Ser Leu Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro
12845 12850 12855

Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
12860 12865 12870

Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
12875 12880 12885

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly
12890 12895 12900

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys
12905 12910 12915

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu
12920 12925 12930

Asp Pro Lys Ser Pro Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu
12935 12940 12945

Leu Ser Gln Leu Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr
12950 12955 12960

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Thr
12965 12970 12975

Ser Ala Pro Asn Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
12980 12985 12990

Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Ser Ala
12995 13000 13005

022438.43867(pct2).ST25.txt

Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
 13010 13015 13020
 Leu Gln Tyr Glu Glu Asp Met His His Pro Gly Ser Arg Lys Phe
 13025 13030 13035
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe
 13040 13045 13050
 Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr
 13055 13060 13065
 Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala
 13070 13075 13080
 Ile Cys Ser His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asn Arg
 13085 13090 13095
 Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Gly Ile Lys
 13100 13105 13110
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 13115 13120 13125
 Gly Phe Thr His Arg Ser Ser Val Ala Pro Thr Ser Thr Pro Gly
 13130 13135 13140
 Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu
 13145 13150 13155
 Pro Ser Pro Thr Thr Ala Val Pro Leu Leu Val Pro Phe Thr Leu
 13160 13165 13170
 Asn Phe Thr Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Arg His
 13175 13180 13185
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 13190 13195 13200
 Leu Leu Gly Pro Leu Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr
 13205 13210 13215
 Ser Gly Cys Arg Leu Ile Ser Leu Arg Ser Glu Lys Asp Gly Ala
 13220 13225 13230
 Ala Thr Gly Val Asp Ala Ile Cys Thr His His Leu Asn Pro Gln
 13235 13240 13245

022438.43867(pct2).ST25.txt

Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Gln Leu Ser Gln
 13250 13255 13260
 Met Thr Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 13265 13270 13275
 Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Gly Leu
 13280 13285 13290
 Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly Thr Ser
 13295 13300 13305
 Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly Pro Leu
 13310 13315 13320
 Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 13325 13330 13335
 Glu Glu Asp Met His Arg Pro Gly Ser Arg Lys Phe Asn Ala Thr
 13340 13345 13350
 Glu Arg Val Leu Gln Gly Leu Leu Ser Pro Ile Phe Lys Asn Ser
 13355 13360 13365
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Ser Leu Arg
 13370 13375 13380
 Pro Glu Lys Asp Gly Ala Ala Thr Gly Met Asp Ala Val Cys Leu
 13385 13390 13395
 Tyr His Pro Asn Pro Lys Arg Pro Gly Leu Asp Arg Glu Gln Leu
 13400 13405 13410
 Tyr Trp Glu Leu Ser Gln Leu Thr His Asn Ile Thr Glu Leu Gly
 13415 13420 13425
 Pro Tyr Ser Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr
 13430 13435 13440
 His Gln Asn Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
 13445 13450 13455
 Val Tyr Trp Ala Thr Thr Gly Thr Pro Ser Ser Phe Pro Gly His
 13460 13465 13470
 Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe Asn Phe Thr
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13475 13480 13485

Ile Thr Asn Leu His Tyr Glu Glu Asn Met Gln His Pro Gly Ser
13490 13495 13500

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys
13505 13510 13515

Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
13520 13525 13530

Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly
13535 13540 13545

Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly
13550 13555 13560

Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His
13565 13570 13575

Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
13580 13585 13590

Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser
13595 13600 13605

Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro
13610 13615 13620

Ser Ser Phe Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro
13625 13630 13635

Phe Thr Phe Asn Phe Thr Ile Thr Asn Leu His Tyr Glu Glu Asn
13640 13645 13650

Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
13655 13660 13665

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
13670 13675 13680

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys
13685 13690 13695

His Glu Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val
13700 13705 13710

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Asp Pro 13715	Ile Gly Pro Gly 13720	Leu Asp Arg Glu Arg 13725	Leu Tyr Trp Glu
Leu Ser 13730	Gln Leu Thr Asn Ser 13735	Ile Thr Glu Leu Gly 13740	Pro Tyr Thr
Leu Asp 13745	Arg Asp Ser Leu Tyr 13750	Val Asn Gly Phe Asn 13755	Pro Arg Ser
Ser Val 13760	Pro Thr Thr Ser Thr 13765	Pro Gly Thr Ser Thr 13770	Val His Leu
Ala Thr 13775	Ser Gly Thr Pro Ser 13780	Ser Leu Pro Gly His 13785	Thr Ala Pro
Val Pro 13790	Leu Leu Ile Pro Phe 13795	Thr Leu Asn Phe Thr 13800	Ile Thr Asn
Leu His 13805	Tyr Glu Glu Asn Met 13810	Gln His Pro Gly Ser 13815	Arg Lys Phe
Asn Thr 13820	Thr Glu Arg Val Leu 13825	Gln Gly Leu Leu Lys 13830	Pro Leu Phe
Lys Asn 13835	Thr Ser Val Gly Pro 13840	Leu Tyr Ser Gly Cys 13845	Arg Leu Thr
Leu Leu 13850	Arg Pro Glu Lys His 13855	Glu Ala Ala Thr Gly 13860	Val Asp Thr
Ile Cys 13865	Thr His Arg Val Asp 13870	Pro Ile Gly Pro Gly 13875	Leu Asp Arg
Glu Xaa 13880	Leu Tyr Trp Glu Leu 13885	Ser Xaa Leu Thr Xaa 13890	Xaa Ile Xaa
Glu Leu 13895	Gly Pro Tyr Xaa Leu 13900	Asp Arg Xaa Ser Leu 13905	Tyr Val Asn
Gly Phe 13910	Xaa Xaa Xaa Xaa Xaa 13915	Xaa Xaa Xaa Thr Ser 13920	Thr Pro Gly
Thr Ser 13925	Xaa Val Xaa Leu Xaa 13930	Thr Ser Gly Thr Pro 13935	Xaa Xaa Xaa
Pro Xaa 13940	Xaa Thr Ser Ala Gly 13945	Pro Leu Leu Val Pro 13950	Phe Thr Leu

022438.43867(pct2).ST25.txt

Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His
 13955 13960 13965
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 13970 13975 13980
 Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr
 13985 13990 13995
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala
 14000 14005 14010
 Ala Thr Gly Met Asp Ala Ile Cys Ser His Arg Leu Asp Pro Lys
 14015 14020 14025
 Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln
 14030 14035 14040
 Leu Thr His Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 14045 14050 14055
 Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Ala
 14060 14065 14070
 Pro Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser
 14075 14080 14085
 Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala Val Pro Leu
 14090 14095 14100
 Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr
 14105 14110 14115
 Gly Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 14120 14125 14130
 Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Leu Phe Lys Asn Ser
 14135 14140 14145
 Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Ile Ser Leu Arg
 14150 14155 14160
 Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
 14165 14170 14175
 His His Leu Asn Pro Gln Ser Pro Gly Leu Asp Arg Glu Gln Leu
 14180 14185 14190

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Tyr Trp Gln Leu Ser Gln Met Thr Asn Gly Ile Lys Glu Leu Gly
 14195 14200 14205
 Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
 14210 14215 14220
 His Arg Ser Ser Gly Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr
 14225 14230 14235
 Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro
 14240 14245 14250
 Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
 14255 14260 14265
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser
 14270 14275 14280
 Arg Lys Phe Asn Ala Thr Glu Arg Val Leu Gln Gly Leu Leu Ser
 14285 14290 14295
 Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
 14300 14305 14310
 Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly
 14315 14320 14325
 Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly
 14330 14335 14340
 Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His
 14345 14350 14355
 Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
 14360 14365 14370
 Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr Thr Arg
 14375 14380 14385
 Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg Thr Pro
 14390 14395 14400
 Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu Val Leu
 14405 14410 14415
 Phe Thr Ile Asn Cys Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp
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14420 14425 14430

Met Arg Arg Thr Gly Ser Arg Lys Phe Asn Thr Met Glu Ser Val
 14435 14440 14445

Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser Val Gly
 14450 14455 14460

Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Lys Lys
 14465 14470 14475

Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu
 14480 14485 14490

Asp Pro Lys Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu
 14495 14500 14505

Leu Ser Lys Leu Thr Asn Asp Ile Glu Glu Leu Gly Pro Tyr Thr
 14510 14515 14520

Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser
 14525 14530 14535

Ser Val Ser Thr Thr Ser Thr Pro Gly Thr Ser Thr Val Asp Leu
 14540 14545 14550

Arg Thr Ser Gly Thr Pro Ser Ser Leu Ser Ser Pro Thr Ile Met
 14555 14560 14565

Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile
 14570 14575 14580

Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg
 14585 14590 14595

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro
 14600 14605 14610

Leu Phe Lys Asn Thr Ser Val Ser Ser Leu Tyr Ser Gly Cys Arg
 14615 14620 14625

Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Arg Val
 14630 14635 14640

Asp Ala Ala Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu
 14645 14650 14655

022438.43867(pct2).ST25.txt

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser
 14660 14665 14670

Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Val Ser Leu Tyr
 14675 14680 14685

Val Asn Gly Phe Asn Pro Arg Ser Ser Val Pro Thr Thr Ser Thr
 14690 14695 14700

Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser
 14705 14710 14715

Ser Leu Pro Gly His Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe
 14720 14725 14730

Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met
 14735 14740 14745

Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 14750 14755 14760

Gln Gly Leu Leu Lys Pro Leu Phe Arg Asn Ser Ser Leu Glu Tyr
 14765 14770 14775

Leu Tyr Ser Gly Cys Arg Leu Ala Ser Leu Arg Pro Glu Lys Asp
 14780 14785 14790

Ser Ser Ala Met Ala Val Asp Ala Ile Cys Thr His Arg Pro Asp
 14795 14800 14805

Pro Glu Asp Leu Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu
 14810 14815 14820

Ser Asn Leu Thr Asn Gly Ile Gln Glu Leu Gly Pro Tyr Thr Leu
 14825 14830 14835

Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser
 14840 14845 14850

Phe Leu Thr Thr Ser Thr Pro Trp Thr Ser Thr Val Asp Leu Gly
 14855 14860 14865

Thr Ser Gly Thr Pro Ser Pro Val Pro Ser Pro Thr Thr Ala Gly
 14870 14875 14880

Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu
 14885 14890 14895

022438.43867(pct2).ST25.txt

Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser Arg Arg Phe Asn
 14900 14905 14910
 Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Thr Pro Leu Phe Lys
 14915 14920 14925
 Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu
 14930 14935 14940
 Leu Arg Pro Glu Lys Gln Glu Ala Ala Thr Gly Val Asp Thr Ile
 14945 14950 14955
 Cys Thr His Arg Val Asp Pro Ile Gly Pro Gly Leu Asp Arg Glu
 14960 14965 14970
 Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu
 14975 14980 14985
 Leu Gly Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly
 14990 14995 15000
 Phe Asn Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr
 15005 15010 15015
 Ser Thr Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro
 15020 15025 15030
 Gly His Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn
 15035 15040 15045
 Phe Thr Ile Thr Asp Leu His Tyr Glu Glu Asn Met Gln His Pro
 15050 15055 15060
 Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
 15065 15070 15075
 Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser
 15080 15085 15090
 Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala Ala
 15095 15100 15105
 Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr Gly
 15110 15115 15120
 Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu
 15125 15130 15135

022438.43867(pct2).ST25.txt

Thr Asn Ser Val Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asp
15140 15145 15150

Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr
15155 15160 15165

Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly
15170 15175 15180

Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu
15185 15190 15195

Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu
15200 15205 15210

Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe Ser Thr Thr Glu
15215 15220 15225

Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Asn Thr Ser
15230 15235 15240

Val Ser Ser Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
15245 15250 15255

Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr His
15260 15265 15270

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Arg Leu Tyr
15275 15280 15285

Trp Lys Leu Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro
15290 15295 15300

Tyr Thr Leu Asp Arg His Ser Leu Tyr Val Asn Gly Phe Thr His
15305 15310 15315

Gln Ser Ser Met Thr Thr Thr Arg Thr Pro Asp Thr Ser Thr Met
15320 15325 15330

His Leu Ala Thr Ser Arg Thr Pro Ala Ser Leu Ser Gly Pro Thr
15335 15340 15345

Thr Ala Ser Pro Leu Leu Val Leu Phe Thr Ile Asn Phe Thr Ile
15350 15355 15360

Thr Asn Gln Arg Tyr Glu Glu Asn Met His His Pro Gly Ser Arg
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15365 15370 15375

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro
15380 15385 15390

Val Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
15395 15400 15405

Leu Thr Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val
15410 15415 15420

Asp Ala Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu
15425 15430 15435

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser
15440 15445 15450

Ile Thr Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr
15455 15460 15465

Val Asn Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile
15470 15475 15480

Pro Gly Thr Ser Ala Val His Leu Glu Thr Ser Gly Thr Pro Ala
15485 15490 15495

Ser Leu Pro Gly His Thr Ala Pro Gly Pro Leu Leu Val Pro Phe
15500 15505 15510

Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met
15515 15520 15525

Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
15530 15535 15540

Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr Ser Val Gly Pro
15545 15550 15555

Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Arg
15560 15565 15570

Gly Ala Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Leu Asp
15575 15580 15585

Pro Leu Asn Pro Gly Leu Asp Arg Glu Gln Leu Tyr Trp Glu Leu
15590 15595 15600

022438.43867(pct2).ST25.txt

Ser Lys 15605 Leu Thr Arg Gly Ile 15610 Ile Glu Leu Gly Pro 15615 Tyr Leu Leu
 Asp Arg 15620 Gly Ser Leu Tyr Val 15625 Asn Gly Phe Thr His 15630 Arg Thr Ser
 Val 15635 Thr Thr Ser Thr Pro 15640 Gly Thr Ser Thr Val 15645 Asp Leu Gly
 Thr Ser 15650 Gly Thr Pro Phe Ser 15655 Leu Pro Ser Pro Ala 15660 Xaa Xaa Xaa
 Pro Leu 15665 Leu Xaa Pro Phe Thr 15670 Leu Asn Phe Thr Ile 15675 Thr Asn Leu
 Xaa Tyr 15680 Glu Glu Xaa Met Xaa 15685 Xaa Pro Gly Ser Arg 15690 Lys Phe Asn
 Thr Thr 15695 Glu Arg Val Leu Gln 15700 Thr Leu Leu Gly Pro 15705 Met Phe Lys
 Asn Thr 15710 Ser Val Gly Leu Leu 15715 Tyr Ser Gly Cys Arg 15720 Leu Thr Leu
 Leu Arg 15725 Ser Glu Lys Asp Gly 15730 Ala Ala Thr Gly Val 15735 Asp Ala Ile
 Cys Thr 15740 His Arg Leu Asp Pro 15745 Lys Ser Pro Gly Val 15750 Asp Arg Glu
 Gln Leu 15755 Tyr Trp Glu Leu Ser 15760 Gln Leu Thr Asn Gly 15765 Ile Lys Glu
 Leu Gly 15770 Pro Tyr Thr Leu Asp 15775 Arg Asn Ser Leu Tyr 15780 Val Asn Gly
 Phe Thr 15785 His Trp Ile Pro Val 15790 Pro Thr Ser Ser Thr 15795 Pro Gly Thr
 Ser Thr 15800 Val Asp Leu Gly Ser 15805 Gly Thr Pro Ser Leu 15810 Pro Ser Ser
 Pro Thr 15815 Thr Ala Gly Pro Leu 15820 Leu Val Pro Phe Thr 15825 Leu Asn Phe
 Thr Ile 15830 Thr Asn Leu Lys Tyr 15835 Glu Glu Asp Met His 15840 Cys Pro Gly

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Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu
 15845 15850 15855
 Gly Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly
 15860 15865 15870
 Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr
 15875 15880 15885
 Gly Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro
 15890 15895 15900
 Gly Val Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr
 15905 15910 15915
 Asn Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser
 15920 15925 15930
 Leu Tyr Val Asn Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr
 15935 15940 15945
 Ser Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr
 15950 15955 15960
 Pro Ser Ser Leu Pro Ser Pro Thr Xaa Xaa Xaa Pro Leu Leu Xaa
 15965 15970 15975
 Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu
 15980 15985 15990
 Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg
 15995 16000 16005
 Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val
 16010 16015 16020
 Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu
 16025 16030 16035
 Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa
 16040 16045 16050
 Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp
 16055 16060 16065
 Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr
 16070 16075 16080

022438.43867(pct2).ST25.txt

Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr His Trp
 16085 16090 16095
 Ile Pro Val Pro Thr Ser Ser Thr Pro Gly Thr Ser Thr Val Asp
 16100 16105 16110
 Leu Gly Ser Gly Thr Pro Ser Ser Leu Pro Ser Pro Thr Thr Ala
 16115 16120 16125
 Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
 16130 16135 16140
 Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly Ser Arg Lys Phe
 16145 16150 16155
 Asn Thr Thr Glu Arg Val Leu Gln Ser Leu Leu Gly Pro Met Phe
 16160 16165 16170
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 16175 16180 16185
 Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly Val Asp Ala
 16190 16195 16200
 Ile Cys Thr His Arg Val Asp Pro Lys Ser Pro Gly Val Asp Arg
 16205 16210 16215
 Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn Gly Ile Lys
 16220 16225 16230
 Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn
 16235 16240 16245
 Gly Phe Thr His Gln Thr Ser Ala Pro Asn Thr Ser Thr Pro Gly
 16250 16255 16260
 Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu
 16265 16270 16275
 Pro Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu
 16280 16285 16290
 Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His
 16295 16300 16305
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
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Pro Tyr Thr Leu Asp Arg Asn Ser Leu Tyr Val Asn Gly Phe Thr
 16550 16555 16560
 His Arg Ser Ser Met Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
 16565 16570 16575
 Val Asp Val Gly Thr Ser Gly Thr Pro Ser Ser Ser Pro Ser Pro
 16580 16585 16590
 Thr Thr Ala Gly Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr
 16595 16600 16605
 Ile Thr Asn Leu Gln Tyr Gly Glu Asp Met Gly His Pro Gly Ser
 16610 16615 16620
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Gly
 16625 16630 16635
 Pro Ile Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
 16640 16645 16650
 Arg Leu Thr Ser Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
 16655 16660 16665
 Val Asp Ala Ile Cys Ile His His Leu Asp Pro Lys Ser Pro Gly
 16670 16675 16680
 Leu Asn Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln Leu Thr Asn
 16685 16690 16695
 Gly Ile Lys Glu Leu Gly Pro Tyr Thr Leu Asp Arg Asn Ser Leu
 16700 16705 16710
 Tyr Val Asn Gly Phe Thr His Arg Thr Ser Val Pro Thr Thr Ser
 16715 16720 16725
 Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro
 16730 16735 16740
 Phe Ser Leu Pro Ser Pro Ala Thr Ala Gly Pro Leu Leu Val Leu
 16745 16750 16755
 Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Lys Tyr Glu Glu Asp
 16760 16765 16770
 Met His Arg Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
 16775 16780 16785

022438.43867(pct2).ST25.txt

Leu Gln Thr Leu Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly
 16790 16795 16800
 Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Ser Glu Lys
 16805 16810 16815
 Asp Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Leu
 16820 16825 16830
 Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
 16835 16840 16845
 Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa
 16850 16855 16860
 Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa
 16865 16870 16875
 Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu
 16880 16885 16890
 Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa
 16895 16900 16905
 Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
 16910 16915 16920
 Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe
 16925 16930 16935
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe
 16940 16945 16950
 Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 16955 16960 16965
 Leu Leu Arg Pro Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala
 16970 16975 16980
 Ile Cys Thr Tyr Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg
 16985 16990 16995
 Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr
 17000 17005 17010
 Glu Leu Gly Pro Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Val Asn
 17015 17020 17025

022438.43867(pct2).ST25.txt

Gly Phe Thr His Arg Ser Ser Val Pro Thr Thr Ser Ile Pro Gly
 17030 17035 17040
 Thr Ser Ala Val His Leu Glu Thr Thr Gly Thr Pro Ser Ser Phe
 17045 17050 17055
 Pro Gly His Thr Glu Pro Gly Pro Leu Leu Ile Pro Phe Thr Phe
 17060 17065 17070
 Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His
 17075 17080 17085
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 17090 17095 17100
 Leu Leu Thr Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr
 17105 17110 17115
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Gln Glu Ala
 17120 17125 17130
 Ala Thr Gly Val Asp Thr Ile Cys Thr His Arg Val Asp Pro Ile
 17135 17140 17145
 Gly Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Glu Leu Ser Gln
 17150 17155 17160
 Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg
 17165 17170 17175
 Asp Ser Leu Tyr Val Asp Gly Phe Asn Pro Trp Ser Ser Val Pro
 17180 17185 17190
 Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser
 17195 17200 17205
 Gly Thr Pro Ser Pro Leu Pro Gly His Thr Ala Pro Val Pro Leu
 17210 17215 17220
 Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asp Leu His Tyr
 17225 17230 17235
 Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 17240 17245 17250
 Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe Lys Ser Thr
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17255 17260 17265

Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
17270 17275 17280

Pro Glu Lys His Gly Ala Ala Thr Gly Val Asp Ala Ile Cys Thr
17285 17290 17295

Leu Arg Leu Asp Pro Thr Gly Pro Gly Leu Asp Arg Glu Arg Leu
17300 17305 17310

Tyr Trp Glu Leu Ser Gln Leu Thr Asn Ser Ile Thr Glu Leu Gly
17315 17320 17325

Pro Tyr Thr Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Asn
17330 17335 17340

Pro Trp Ser Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
17345 17350 17355

Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His
17360 17365 17370

Thr Thr Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr
17375 17380 17385

Ile Thr Asn Leu Lys Tyr Glu Glu Asp Met His Cys Pro Gly Ser
17390 17395 17400

Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Ser Leu His Gly
17405 17410 17415

Pro Met Phe Lys Asn Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys
17420 17425 17430

Arg Leu Thr Leu Leu Arg Ser Glu Lys Asp Gly Ala Ala Thr Gly
17435 17440 17445

Val Asp Ala Ile Cys Thr His Arg Leu Asp Pro Lys Ser Pro Gly
17450 17455 17460

Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa
17465 17470 17475

Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
17480 17485 17490

022438.43867(pct2).ST25.txt

Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser
 17495 17500 17505
 Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro
 17510 17515 17520
 Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro
 17525 17530 17535
 Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa
 17540 17545 17550
 Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
 17555 17560 17565
 Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly
 17570 17575 17580
 Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys
 17585 17590 17595
 Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa
 17600 17605 17610
 Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu
 17615 17620 17625
 Leu Ser Xaa Leu Thr Asn Ser Ile Thr Glu Leu Gly Pro Tyr Thr
 17630 17635 17640
 Leu Asp Arg Asp Ser Leu Tyr Val Asn Gly Phe Thr His Arg Ser
 17645 17650 17655
 Ser Met Pro Thr Thr Ser Ile Pro Gly Thr Ser Ala Val His Leu
 17660 17665 17670
 Glu Thr Ser Gly Thr Pro Ala Ser Leu Pro Gly His Thr Ala Pro
 17675 17680 17685
 Gly Pro Leu Leu Val Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn
 17690 17695 17700
 Leu Gln Tyr Glu Glu Asp Met Arg His Pro Gly Ser Arg Lys Phe
 17705 17710 17715
 Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Lys Pro Leu Phe
 17720 17725 17730

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Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr
 17735 17740 17745
 Leu Leu Arg Pro Glu Lys Arg Gly Ala Ala Thr Gly Val Asp Thr
 17750 17755 17760
 Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu Asp Arg
 17765 17770 17775
 Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa
 17780 17785 17790
 Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn
 17795 17800 17805
 Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly
 17810 17815 17820
 Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa
 17825 17830 17835
 Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu
 17840 17845 17850
 Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa
 17855 17860 17865
 Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly
 17870 17875 17880
 Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr
 17885 17890 17895
 Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala
 17900 17905 17910
 Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa
 17915 17920 17925
 Xaa Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa
 17930 17935 17940
 Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg
 17945 17950 17955
 Xaa Ser Leu Tyr Val Asn Gly Phe His Pro Arg Ser Ser Val Pro
 17960 17965 17970

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Thr Thr Ser Thr Pro Gly Thr Ser Thr Val His Leu Ala Thr Ser
 17975 17980 17985
 Gly Thr Pro Ser Ser Leu Pro Gly His Thr Ala Pro Val Pro Leu
 17990 17995 18000
 Leu Ile Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu His Tyr
 18005 18010 18015
 Glu Glu Asn Met Gln His Pro Gly Ser Arg Lys Phe Asn Thr Thr
 18020 18025 18030
 Glu Arg Val Leu Gln Gly Leu Leu Gly Pro Met Phe Lys Asn Thr
 18035 18040 18045
 Ser Val Gly Leu Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
 18050 18055 18060
 Pro Glu Lys Asn Gly Ala Ala Thr Gly Met Asp Ala Ile Cys Ser
 18065 18070 18075
 His Arg Leu Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu
 18080 18085 18090
 Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly
 18095 18100 18105
 Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa
 18110 18115 18120
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa
 18125 18130 18135
 Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa
 18140 18145 18150
 Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr
 18155 18160 18165
 Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser
 18170 18175 18180
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa
 18185 18190 18195
 Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys

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18200		18205		18210							
Arg	Leu	Thr	Leu	Leu	Arg	Xaa	Glu	Lys	Xaa	Xaa	Ala
18215						18220					18225
											Ala
											Thr
											Xaa
Val	Asp	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Asp	Pro	Xaa
18230						18235					18240
											Xaa
											Pro
											Gly
Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa
18245						18250					18255
											Leu
											Thr
											Xaa
Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg
18260						18265					18270
											Xaa
											Ser
											Leu
Tyr	Val	Asn	Gly	Phe	Thr	His	Gln	Asn	Ser	Val	Pro
18275						18280					18285
											Thr
											Thr
											Ser
Thr	Pro	Gly	Thr	Ser	Thr	Val	Tyr	Trp	Ala	Thr	Thr
18290						18295					18300
											Gly
											Thr
											Pro
Ser	Ser	Phe	Pro	Gly	His	Thr	Glu	Pro	Gly	Pro	Leu
18305						18310					18315
											Leu
											Ile
											Pro
Phe	Thr	Phe	Asn	Phe	Thr	Ile	Thr	Asn	Leu	His	Tyr
18320						18325					18330
											Glu
											Glu
											Asn
Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
18335						18340					18345
											Glu
											Arg
											Val
Leu	Gln	Gly	Leu	Leu	Thr	Pro	Leu	Phe	Lys	Asn	Thr
18350						18355					18360
											Ser
											Val
											Gly
Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
18365						18370					18375
											Pro
											Glu
											Lys
Gln	Glu	Ala	Ala	Thr	Gly	Val	Asp	Thr	Ile	Cys	Thr
18380						18385					18390
											His
											Arg
											Val
Asp	Pro	Ile	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu
18395						18400					18405
											Tyr
											Trp
											Glu
Leu	Ser	Xaa	Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly
18410						18415					18420
											Pro
											Tyr
											Xaa
Leu	Asp	Arg	Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Xaa
18425						18430					18435
											Xaa
											Xaa
											Xaa

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Xaa Xaa	Xaa Xaa Thr Ser Thr	Pro Gly Thr Ser Xaa	Val Xaa Leu
18440	18445	18450	
Xaa Thr	Ser Gly Thr Pro Xaa	Xaa Xaa Pro Xaa Xaa	Thr Xaa Xaa
18455	18460	18465	
Xaa Pro	Leu Leu Xaa Pro Phe	Thr Leu Asn Phe Thr	Ile Thr Asn
18470	18475	18480	
Leu Xaa	Tyr Glu Glu Xaa Met	Xaa Xaa Pro Gly Ser	Arg Lys Phe
18485	18490	18495	
Asn Thr	Thr Glu Arg Val Leu	Gln Gly Leu Leu Xaa	Pro Xaa Phe
18500	18505	18510	
Lys Xaa	Thr Ser Val Gly Xaa	Leu Tyr Ser Gly Cys	Arg Leu Thr
18515	18520	18525	
Leu Leu	Arg Xaa Glu Lys Xaa	Xaa Ala Ala Thr Xaa	Val Asp Xaa
18530	18535	18540	
Xaa Cys	Xaa Xaa Xaa Xaa Asp	Pro Xaa Xaa Pro Gly	Leu Asp Arg
18545	18550	18555	
Glu Xaa	Leu Tyr Trp Glu Leu	Ser Xaa Leu Thr Xaa	Xaa Ile Xaa
18560	18565	18570	
Glu Leu	Gly Pro Tyr Xaa Leu	Asp Arg Xaa Ser Leu	Tyr Val Asn
18575	18580	18585	
Gly Phe	Thr His Arg Ser Ser	Val Pro Thr Thr Ser	Ser Pro Gly
18590	18595	18600	
Thr Ser	Thr Val His Leu Ala	Thr Ser Gly Thr Pro	Ser Ser Leu
18605	18610	18615	
Pro Gly	His Thr Ala Pro Val	Pro Leu Leu Ile Pro	Phe Thr Leu
18620	18625	18630	
Asn Phe	Thr Ile Thr Asn Leu	His Tyr Glu Glu Asn	Met Gln His
18635	18640	18645	
Pro Gly	Ser Arg Lys Phe Asn	Thr Thr Glu Arg Val	Leu Gln Gly
18650	18655	18660	
Leu Leu	Lys Pro Leu Phe Lys	Ser Thr Ser Val Gly	Pro Leu Tyr
18665	18670	18675	

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Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys His Gly Ala
 18680 18685 18690
 Ala Thr Gly Val Asp Ala Ile Cys Thr Leu Arg Leu Asp Pro Thr
 18695 18700 18705
 Gly Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa
 18710 18715 18720
 Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg
 18725 18730 18735
 Xaa Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 18740 18745 18750
 Xaa Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser
 18755 18760 18765
 Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa Thr Xaa Xaa Xaa Pro Leu
 18770 18775 18780
 Leu Xaa Pro Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr
 18785 18790 18795
 Glu Glu Xaa Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr
 18800 18805 18810
 Glu Arg Val Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr
 18815 18820 18825
 Ser Val Gly Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg
 18830 18835 18840
 Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa Cys Xaa
 18845 18850 18855
 Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu Xaa Leu
 18860 18865 18870
 Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly
 18875 18880 18885
 Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Thr
 18890 18895 18900
 His Arg Thr Ser Val Pro Thr Thr Ser Thr Pro Gly Thr Ser Thr
 18905 18910 18915

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Val His Leu Ala Thr Ser Gly Thr Pro Ser Ser Leu Pro Gly His
 18920 18925 18930
 Thr Ala Pro Val Pro Leu Leu Ile Pro Phe Thr Leu Asn Phe Thr
 18935 18940 18945
 Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His Arg Pro Gly Ser
 18950 18955 18960
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Ser
 18965 18970 18975
 Pro Ile Phe Lys Asn Ser Ser Val Gly Pro Leu Tyr Ser Gly Cys
 18980 18985 18990
 Arg Leu Thr Ser Leu Arg Pro Glu Lys Asp Gly Ala Ala Thr Gly
 18995 19000 19005
 Met Asp Ala Val Cys Leu Tyr His Pro Asn Pro Lys Arg Pro Gly
 19010 19015 19020
 Leu Asp Arg Glu Gln Leu Tyr Cys Glu Leu Ser Gln Leu Thr His
 19025 19030 19035
 Asn Ile Thr Glu Leu Gly Pro Tyr Ser Leu Asp Arg Asp Ser Leu
 19040 19045 19050
 Tyr Val Asn Gly Phe Thr His Gln Asn Ser Val Pro Thr Thr Ser
 19055 19060 19065
 Thr Pro Gly Thr Ser Thr Val Tyr Trp Ala Thr Thr Gly Thr Pro
 19070 19075 19080
 Ser Ser Phe Pro Gly His Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro
 19085 19090 19095
 Phe Thr Leu Asn Phe Thr Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa
 19100 19105 19110
 Met Xaa Xaa Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val
 19115 19120 19125
 Leu Gln Gly Leu Leu Xaa Pro Xaa Phe Lys Xaa Thr Ser Val Gly
 19130 19135 19140
 Xaa Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Xaa Glu Lys
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19145		19150		19155	
Xaa Xaa	Ala Ala Thr Xaa	Val	Asp Xaa Xaa Cys	Xaa	Xaa Xaa Xaa
19160		19165		19170	
Asp Pro	Xaa Xaa Pro Gly	Leu	Asp Arg Glu Xaa	Leu	Tyr Trp Glu
19175		19180		19185	
Leu Ser	Xaa Leu Thr Xaa	Xaa	Ile Xaa Glu Leu	Gly	Pro Tyr Xaa
19190		19195		19200	
Leu Asp	Arg Xaa Ser Leu	Tyr	Val Asn Gly Phe	Thr	His Trp Ser
19205		19210		19215	
Ser Gly	Leu Thr Thr Ser	Thr	Pro Trp Thr Ser	Thr	Val Asp Leu
19220		19225		19230	
Gly Thr	Ser Gly Thr Pro	Ser	Pro Val Pro Ser	Pro	Thr Thr Ala
19235		19240		19245	
Gly Pro	Leu Leu Val Pro	Phe	Thr Leu Asn Phe	Thr	Ile Thr Asn
19250		19255		19260	
Leu Gln	Tyr Glu Glu Asp	Met	His Arg Pro Gly	Ser	Arg Lys Phe
19265		19270		19275	
Asn Ala	Thr Glu Arg Val	Leu	Gln Gly Leu Leu	Ser	Pro Ile Phe
19280		19285		19290	
Lys Asn	Thr Ser Val Gly	Pro	Leu Tyr Ser Gly	Cys	Arg Leu Thr
19295		19300		19305	
Leu Leu	Arg Pro Glu Lys	Gln	Glu Ala Ala Thr	Gly	Val Asp Thr
19310		19315		19320	
Ile Cys	Thr His Arg Val	Asp	Pro Ile Gly Pro	Gly	Leu Asp Arg
19325		19330		19335	
Glu Xaa	Leu Tyr Trp Glu	Leu	Ser Xaa Leu Thr	Xaa	Xaa Ile Xaa
19340		19345		19350	
Glu Leu	Gly Pro Tyr Xaa	Leu	Asp Arg Xaa Ser	Leu	Tyr Val Asn
19355		19360		19365	
Gly Phe	Xaa Xaa Xaa Xaa	Xaa	Xaa Xaa Xaa Thr	Ser	Thr Pro Gly
19370		19375		19380	

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Thr	Ser	Xaa	Val	Xaa	Leu	Xaa	Thr	Ser	Gly	Thr	Pro	Xaa	Xaa	Xaa
19385						19390					19395			
Pro	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Pro	Leu	Leu	Xaa	Pro	Phe	Thr	Leu
19400						19405					19410			
Asn	Phe	Thr	Ile	Thr	Asn	Leu	Xaa	Tyr	Glu	Glu	Xaa	Met	Xaa	Xaa
19415						19420					19425			
Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly
19430						19435					19440			
Leu	Leu	Xaa	Pro	Xaa	Phe	Lys	Xaa	Thr	Ser	Val	Gly	Xaa	Leu	Tyr
19445						19450					19455			
Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Xaa	Glu	Lys	Xaa	Xaa	Ala
19460						19465					19470			
Ala	Thr	Xaa	Val	Asp	Xaa	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Asp	Pro	Xaa
19475						19480					19485			
Xaa	Pro	Gly	Leu	Asp	Arg	Glu	Xaa	Leu	Tyr	Trp	Glu	Leu	Ser	Xaa
19490						19495					19500			
Leu	Thr	Xaa	Xaa	Ile	Xaa	Glu	Leu	Gly	Pro	Tyr	Xaa	Leu	Asp	Arg
19505						19510					19515			
Xaa	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	His	Arg	Ser	Phe	Gly	Leu
19520						19525					19530			
Thr	Thr	Ser	Thr	Pro	Trp	Thr	Ser	Thr	Val	Asp	Leu	Gly	Thr	Ser
19535						19540					19545			
Gly	Thr	Pro	Ser	Pro	Val	Pro	Ser	Pro	Thr	Thr	Ala	Gly	Pro	Leu
19550						19555					19560			
Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	Gln	Tyr
19565						19570					19575			
Glu	Glu	Asp	Met	His	Arg	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr
19580						19585					19590			
Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Thr	Pro	Leu	Phe	Arg	Asn	Thr
19595						19600					19605			
Ser	Val	Ser	Ser	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg
19610						19615					19620			

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Pro Glu Lys Asp Gly Ala Ala Thr Arg Val Asp Ala Val Cys Thr
 19625 19630 19635
 His Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Xaa Leu
 19640 19645 19650
 Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu Leu Gly
 19655 19660 19665
 Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly Phe Xaa
 19670 19675 19680
 Xaa Xaa Xaa Xaa Xaa Xaa Thr Ser Thr Pro Gly Thr Ser Xaa
 19685 19690 19695
 Val Xaa Leu Xaa Thr Ser Gly Thr Pro Xaa Xaa Xaa Pro Xaa Xaa
 19700 19705 19710
 Thr Xaa Xaa Xaa Pro Leu Leu Xaa Pro Phe Thr Leu Asn Phe Thr
 19715 19720 19725
 Ile Thr Asn Leu Xaa Tyr Glu Glu Xaa Met Xaa Xaa Pro Gly Ser
 19730 19735 19740
 Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Xaa
 19745 19750 19755
 Pro Xaa Phe Lys Xaa Thr Ser Val Gly Xaa Leu Tyr Ser Gly Cys
 19760 19765 19770
 Arg Leu Thr Leu Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa
 19775 19780 19785
 Val Asp Xaa Xaa Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly
 19790 19795 19800
 Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa
 19805 19810 19815
 Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu
 19820 19825 19830
 Tyr Val Asn Gly Phe Thr His Trp Ile Pro Val Pro Thr Ser Ser
 19835 19840 19845
 Thr Pro Gly Thr Ser Thr Val Asp Leu Gly Ser Gly Thr Pro Ser
 19850 19855 19860

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Ser Leu 19865 Pro Ser Pro Thr Thr 19870 Ala Gly Pro Leu Leu 19875 Val Pro Phe
 Thr Leu 19880 Asn Phe Thr Ile Thr 19885 Asn Leu Gln Tyr Gly 19890 Glu Asp Met
 Gly His 19895 Pro Gly Ser Arg Lys 19900 Phe Asn Thr Thr Glu 19905 Arg Val Leu
 Gln Gly 19910 Leu Leu Gly Pro Ile 19915 Phe Lys Asn Thr Ser 19920 Val Gly Pro
 Leu Tyr 19925 Ser Gly Cys Arg Leu 19930 Thr Ser Leu Arg Ser 19935 Glu Lys Asp
 Gly Ala 19940 Ala Thr Gly Val Asp 19945 Ala Ile Cys Ile His 19950 His Leu Asp
 Pro Lys 19955 Ser Pro Gly Leu Asp 19960 Arg Glu Xaa Leu Tyr 19965 Trp Glu Leu
 Ser Xaa 19970 Leu Thr Xaa Xaa Ile 19975 Xaa Glu Leu Gly Pro 19980 Tyr Xaa Leu
 Asp Arg 19985 Xaa Ser Leu Tyr Val 19990 Asn Gly Phe Xaa Xaa 19995 Xaa Xaa Xaa
 Xaa Xaa 20000 Xaa Thr Ser Thr Pro 20005 Gly Thr Ser Xaa Val 20010 Xaa Leu Xaa
 Thr Ser 20015 Gly Thr Pro Xaa Xaa 20020 Xaa Pro Xaa Xaa Thr 20025 Xaa Xaa Xaa
 Pro Leu 20030 Leu Xaa Pro Phe Thr 20035 Leu Asn Phe Thr Ile 20040 Thr Asn Leu
 Xaa Tyr 20045 Glu Glu Xaa Met Xaa 20050 Xaa Pro Gly Ser Arg 20055 Lys Phe Asn
 Thr Thr 20060 Glu Arg Val Leu Gln 20065 Gly Leu Leu Xaa Pro 20070 Xaa Phe Lys
 Xaa Thr 20075 Ser Val Gly Xaa Leu 20080 Tyr Ser Gly Cys Arg 20085 Leu Thr Leu
 Leu Arg Xaa Glu Lys Xaa Xaa Ala Ala Thr Xaa Val Asp Xaa Xaa

20090 022438.43867(pct2).ST25.txt
 20095 20100

Cys Xaa Xaa Xaa Xaa Asp Pro Xaa Xaa Pro Gly Leu Asp Arg Glu
 20105 20110 20115

Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu Thr Xaa Xaa Ile Xaa Glu
 20120 20125 20130

Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa Ser Leu Tyr Val Asn Gly
 20135 20140 20145

Phe Thr His Gln Thr Phe Ala Pro Asn Thr Ser Thr Pro Gly Thr
 20150 20155 20160

Ser Thr Val Asp Leu Gly Thr Ser Gly Thr Pro Ser Ser Leu Pro
 20165 20170 20175

Ser Pro Thr Ser Ala Gly Pro Leu Leu Val Pro Phe Thr Leu Asn
 20180 20185 20190

Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Asp Met His His Pro
 20195 20200 20205

Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu
 20210 20215 20220

Leu Gly Pro Met Phe Lys Asn Thr Ser Val Gly Leu Leu Tyr Ser
 20225 20230 20235

Gly Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asn Gly Ala Ala
 20240 20245 20250

Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser
 20255 20260 20265

Pro Gly Leu Asp Arg Glu Xaa Leu Tyr Trp Glu Leu Ser Xaa Leu
 20270 20275 20280

Thr Xaa Xaa Ile Xaa Glu Leu Gly Pro Tyr Xaa Leu Asp Arg Xaa
 20285 20290 20295

Ser Leu Tyr Val Asn Gly Phe Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20300 20305 20310

Thr Ser Thr Pro Gly Thr Ser Xaa Val Xaa Leu Xaa Thr Ser Gly
 20315 20320 20325

022438.43867(pct2).ST25.txt

Thr	Pro	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Thr	Ala	Pro	Val	Pro	Leu	Leu
	20330					20335					20340			
Ile	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile	Thr	Asn	Leu	His	Tyr	Glu
	20345					20350					20355			
Glu	Asn	Met	Gln	His	Pro	Gly	Ser	Arg	Lys	Phe	Asn	Thr	Thr	Glu
	20360					20365					20370			
Arg	Val	Leu	Gln	Gly	Leu	Leu	Arg	Pro	Leu	Phe	Lys	Ser	Thr	Ser
	20375					20380					20385			
Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg	Leu	Thr	Leu	Leu	Arg	Pro
	20390					20395					20400			
Glu	Lys	His	Gly	Ala	Ala	Thr	Gly	Val	Asp	Ala	Ile	Cys	Thr	Leu
	20405					20410					20415			
Arg	Leu	Asp	Pro	Thr	Gly	Pro	Gly	Leu	Asp	Arg	Glu	Arg	Leu	Tyr
	20420					20425					20430			
Trp	Glu	Leu	Ser	Gln	Leu	Thr	Asn	Ser	Val	Thr	Glu	Leu	Gly	Pro
	20435					20440					20445			
Tyr	Thr	Leu	Asp	Arg	Asp	Ser	Leu	Tyr	Val	Asn	Gly	Phe	Thr	Gln
	20450					20455					20460			
Arg	Ser	Ser	Val	Pro	Thr	Thr	Ser	Ile	Pro	Gly	Thr	Ser	Ala	Val
	20465					20470					20475			
His	Leu	Glu	Thr	Ser	Gly	Thr	Pro	Ala	Ser	Leu	Pro	Gly	His	Thr
	20480					20485					20490			
Ala	Pro	Gly	Pro	Leu	Leu	Val	Pro	Phe	Thr	Leu	Asn	Phe	Thr	Ile
	20495					20500					20505			
Thr	Asn	Leu	Gln	Tyr	Glu	Val	Asp	Met	Arg	His	Pro	Gly	Ser	Arg
	20510					20515					20520			
Lys	Phe	Asn	Thr	Thr	Glu	Arg	Val	Leu	Gln	Gly	Leu	Leu	Lys	Pro
	20525					20530					20535			
Leu	Phe	Lys	Ser	Thr	Ser	Val	Gly	Pro	Leu	Tyr	Ser	Gly	Cys	Arg
	20540					20545					20550			
Leu	Thr	Leu	Leu	Arg	Pro	Glu	Lys	Arg	Gly	Ala	Ala	Thr	Gly	Val
	20555					20560					20565			

022438.43867(pct2).ST25.txt

Asp Thr Ile Cys Thr His Arg Leu Asp Pro Leu Asn Pro Gly Leu
 20570 20575 20580
 Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Lys Leu Thr Arg Gly
 20585 20590 20595
 Ile Ile Glu Leu Gly Pro Tyr Leu Leu Asp Arg Gly Ser Leu Tyr
 20600 20605 20610
 Val Asn Gly Phe Thr His Arg Asn Phe Val Pro Ile Thr Ser Thr
 20615 20620 20625
 Pro Gly Thr Ser Thr Val His Leu Gly Thr Ser Glu Thr Pro Ser
 20630 20635 20640
 Ser Leu Pro Arg Pro Ile Val Pro Gly Pro Leu Leu Val Pro Phe
 20645 20650 20655
 Thr Leu Asn Phe Thr Ile Thr Asn Leu Gln Tyr Glu Glu Ala Met
 20660 20665 20670
 Arg His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu
 20675 20680 20685
 Gln Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Ile Gly Pro
 20690 20695 20700
 Leu Ty Ser Ser Cys Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp
 20705 20710 20715
 Lys Ala Ala Thr Arg Val Asp Ala Ile Cys Thr His His Pro Asp
 20720 20725 20730
 Pro Gln Ser Pro Gly Leu Asn Arg Glu Gln Leu Tyr Trp Glu Leu
 20735 20740 20745
 Ser Gln Leu Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu
 20750 20755 20760
 Asp Arg Asp Ser Leu Tyr Val Asp Gly Phe Thr His Trp Ser Pro
 20765 20770 20775
 Ile Pro Thr Thr Ser Thr Pro Gly Thr Ser Ile Val Asn Leu Gly
 20780 20785 20790
 Thr Ser Gly Ile Pro Pro Ser Leu Pro Glu Thr Thr Xaa Xaa Xaa
 20795 20800 20805

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Pro Leu 20810 Leu Xaa Pro Phe Thr 20815 Leu Asn Phe Thr Ile 20820 Thr Asn Leu
 Xaa Tyr 20825 Glu Glu Xaa Met Xaa 20830 Xaa Pro Gly Ser Arg 20835 Lys Phe Asn
 Thr Thr 20840 Glu Arg Val Leu Gln 20845 Gly Leu Leu Lys Pro 20850 Leu Phe Lys
 Ser Thr 20855 Ser Val Gly Pro Leu 20860 Tyr Ser Gly Cys Arg 20865 Leu Thr Leu
 Leu Arg 20870 Pro Glu Lys Asp Gly 20875 Val Ala Thr Arg Val 20880 Asp Ala Ile
 Cys Thr 20885 His Arg Pro Asp Pro 20890 Lys Ile Pro Gly Leu 20895 Asp Arg Gln
 Gln Leu 20900 Tyr Trp Glu Leu Ser 20905 Gln Leu Thr His Ser 20910 Ile Thr Glu
 Leu Gly 20915 Pro Tyr Thr Leu Asp 20920 Arg Asp Ser Leu Tyr 20925 Val Asn Gly
 Phe Thr 20930 Gln Arg Ser Ser Val 20935 Pro Thr Thr Ser Thr 20940 Pro Gly Thr
 Phe Thr 20945 Val Gln Pro Glu Thr 20950 Ser Glu Thr Pro Ser 20955 Ser Leu Pro
 Gly Pro 20960 Thr Ala Thr Gly Pro 20965 Val Leu Leu Pro Phe 20970 Thr Leu Asn
 Phe Thr 20975 Ile Thr Asn Leu Gln 20980 Tyr Glu Glu Asp Met 20985 His Arg Pro
 Gly Ser 20990 Arg Lys Phe Asn Thr 20995 Thr Glu Arg Val Leu 21000 Gln Gly Leu
 Leu Met 21005 Pro Leu Phe Lys Asn 21010 Thr Ser Val Ser Ser 21015 Leu Tyr Ser
 Gly Cys 21020 Arg Leu Thr Leu Leu 21025 Arg Pro Glu Lys Asp 21030 Gly Ala Ala
 Thr Arg Val Asp Ala Val Cys Thr His Arg Pro Asp Pro Lys Ser
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21035 21040 21045

Pro Gly Leu Asp Arg Glu Arg Leu Tyr Trp Lys Leu Ser Gln Leu
 21050 21055 21060

Thr His Gly Ile Thr Glu Leu Gly Pro Tyr Thr Leu Asp Arg His
 21065 21070 21075

Ser Leu Tyr Val Asn Gly Phe Thr His Gln Ser Ser Met Thr Thr
 21080 21085 21090

Thr Arg Thr Pro Asp Thr Ser Thr Met His Leu Ala Thr Ser Arg
 21095 21100 21105

Thr Pro Ala Ser Leu Ser Gly Pro Thr Thr Ala Ser Pro Leu Leu
 21110 21115 21120

Val Leu Phe Thr Ile Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu
 21125 21130 21135

Glu Asn Met His His Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu
 21140 21145 21150

Arg Val Leu Gln Gly Leu Leu Arg Pro Val Phe Lys Asn Thr Ser
 21155 21160 21165

Val Gly Pro Leu Tyr Ser Gly Cys Arg Leu Thr Leu Leu Arg Pro
 21170 21175 21180

Lys Lys Asp Gly Ala Ala Thr Lys Val Asp Ala Ile Cys Thr Tyr
 21185 21190 21195

Arg Pro Asp Pro Lys Ser Pro Gly Leu Asp Arg Glu Gln Leu Tyr
 21200 21205 21210

Trp Glu Leu Ser Gln Leu Thr His Ser Ile Thr Glu Leu Gly Pro
 21215 21220 21225

Tyr Thr Gln Asp Arg Asp Ser Leu Tyr Asn Val Gly Phe Thr Gln
 21230 21235 21240

Arg Ser Ser Val Pro Thr Thr Ser Val Pro Gly Thr Pro Thr Val
 21245 21250 21255

Asp Leu Gly Thr Ser Gly Thr Pro Val Ser Lys Pro Gly Pro Ser
 21260 21265 21270

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Ala Ala Ser Pro Leu Leu Val Leu Phe Thr Leu Asn Gly Thr Ile
 21275 21280 21285

Thr Asn Leu Arg Tyr Glu Glu Asn Met Gln His Pro Gly Ser Arg
 21290 21295 21300

Lys Phe Asn Thr Thr Glu Arg Val Leu Gln Gly Leu Leu Arg Ser
 21305 21310 21315

Leu Phe Lys Ser Thr Ser Val Gly Pro Leu Tyr Ser Gly Cys Arg
 21320 21325 21330

Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly Thr Ala Thr Gly Val
 21335 21340 21345

Asp Ala Ile Cys Thr His His Pro Asp Pro Lys Ser Pro Arg Leu
 21350 21355 21360

Asp Arg Glu Gln Leu Tyr Trp Glu Leu Ser Gln Leu Thr His Asn
 21365 21370 21375

Ile Thr Glu Leu Gly His Tyr Ala Leu Asp Asn Asp Ser Leu Phe
 21380 21385 21390

Val Asn Gly Phe Thr His Arg Ser Ser Val Ser Thr Thr Ser Thr
 21395 21400 21405

Pro Gly Thr Pro Thr Val Tyr Leu Gly Ala Ser Lys Thr Pro Ala
 21410 21415 21420

Ser Ile Phe Gly Pro Ser Ala Ala Ser His Leu Leu Ile Leu Phe
 21425 21430 21435

Thr Leu Asn Phe Thr Ile Thr Asn Leu Arg Tyr Glu Glu Asn Met
 21440 21445 21450

Trp Pro Gly Ser Arg Lys Phe Asn Thr Thr Glu Arg Val Leu Gln
 21455 21460 21465

Gly Leu Leu Arg Pro Leu Phe Lys Asn Thr Ser Val Gly Pro Leu
 21470 21475 21480

Tyr Ser Gly Ser Arg Leu Thr Leu Leu Arg Pro Glu Lys Asp Gly
 21485 21490 21495

Glu Ala Thr Gly Val Asp Ala Ile Cys Thr His Arg Pro Asp Pro
 21500 21505 21510

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Thr Gly 21515	Pro Gly Leu Asp Arg 21520	Glu Gln Leu Tyr Leu 21525	Glu Leu Ser
Gln Leu 21530	Thr His Ser Ile Thr 21535	Glu Leu Gly Pro Tyr 21540	Thr Leu Asp
Arg Asp 21545	Ser Leu Tyr Val Asn 21550	Gly Phe Thr His Arg 21555	Ser Ser Val
Pro Thr 21560	Thr Ser Thr Gly Val 21565	Val Ser Glu Glu Pro 21570	Phe Thr Leu
Asn Phe 21575	Thr Ile Asn Asn Leu 21580	Arg Tyr Met Ala Asp 21585	Met Gly Gln
Pro Gly 21590	Ser Leu Lys Phe Asn 21595	Ile Thr Asp Asn Val 21600	Met Lys His
Leu Leu 21605	Ser Pro Leu Phe Gln 21610	Arg Ser Ser Leu Gly 21615	Ala Arg Tyr
Thr Gly 21620	Cys Arg Val Ile Ala 21625	Leu Arg Ser Val Lys 21630	Asn Gly Ala
Glu Thr 21635	Arg Val Asp Leu Leu 21640	Cys Thr Tyr Leu Gln 21645	Pro Leu Ser
Gly Pro 21650	Gly Leu Pro Ile Lys 21655	Gln Val Phe His Glu 21660	Leu Ser Gln
Gln Thr 21665	His Gly Ile Thr Arg 21670	Leu Gly Pro Tyr Ser 21675	Leu Asp Lys
Asp Ser 21680	Leu Tyr Leu Asn Gly 21685	Tyr Asn Glu Pro Gly 21690	Leu Asp Glu
Pro Pro 21695	Thr Thr Pro Lys Pro 21700	Ala Thr Thr Phe Leu 21705	Pro Pro Leu
Ser Glu 21710	Ala Thr Thr Ala Met 21715	Gly Tyr His Leu Lys 21720	Thr Leu Thr
Leu Asn 21725	Phe Thr Ile Ser Asn 21730	Leu Gln Tyr Ser Pro 21735	Asp Met Gly
Lys Gly 21740	Ser Ala Thr Phe Asn 21745	Ser Thr Glu Gly Val 21750	Leu Gln His

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Leu Leu Arg Pro Leu. Phe Gln Lys Ser Ser Met Gly Pro Phe Tyr
 21755 21760 21765
 Leu Gly Cys Gln Leu Ile Ser Leu Arg Pro Glu Lys Asp Gly Ala
 21770 21775 21780
 Ala Thr Gly Val Asp Thr Thr Cys Thr Tyr His Pro Asp Pro Val
 21785 21790 21795
 Gly Pro Gly Leu Asp Ile Gln Gln Leu Tyr Trp Glu Leu Ser Gln
 21800 21805 21810
 Leu Thr His Gly Val Thr Gln Leu Gly Phe Tyr Val Leu Asp Arg
 21815 21820 21825
 Asp Ser Leu Phe Ile Asn Gly Tyr Ala Pro Gln Asn Leu Ser Ile
 21830 21835 21840
 Arg Gly Glu Tyr Gln Ile Asn Phe His Ile Val Asn Trp Asn Leu
 21845 21850 21855
 Ser Asn Pro Asp Pro Thr Ser Ser Glu Tyr Ile Thr Leu Leu Arg
 21860 21865 21870
 Asp Ile Gln Asp Lys Val Thr Thr Leu Tyr Lys Gly Ser Gln Leu
 21875 21880 21885
 His Asp Thr Phe Arg Phe Cys Leu Val Thr Asn Leu Thr Met Asp
 21890 21895 21900
 Ser Val Leu Val Thr Val Lys Ala Leu Phe Ser Ser Asn Leu Asp
 21905 21910 21915
 Pro Ser Leu Val Glu Gln Val Phe Leu Asp Lys Thr Leu Asn Ala
 21920 21925 21930
 Ser Phe His Trp Leu Gly Ser Thr Tyr Gln Leu Val Asp Ile His
 21935 21940 21945
 Val Thr Glu Met Glu Ser Ser Val Tyr Gln Pro Thr Ser Ser Ser
 21950 21955 21960
 Ser Thr Gln His Phe Tyr Leu Asn Phe Thr Ile Thr Asn Leu Pro
 21965 21970 21975
 Tyr Ser Gln Asp Lys Ala Gln Pro Gly Thr Thr Asn Tyr Gln Arg
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